

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 27

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: Linear

(i i) MOLECULE TYPE: DNA (genomic)

(v i i) IMMEDIATE SOURCE:

(B) CLONE: Human Fibrinogen A-alpha chain

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(31..84, 1154..1279, 1739..1922, 3055..3200, 3786..5210)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTAGGAGC	CAOCCCCACC	CYTAOAAAAA	ATG TTT TCC ATG AAG ATC GTC TGC	54
			Met Phe Ser Met Arg Ile Val Cys	
			1 5	
CTA GTT CTA AGT GTO GTO GGC ACA GCA TGG GTATGGCCCT TTTCATTTTT				104
Leu Val Leu Ser Val Val Gly Thr Ala Trp				
10	15			
TCTTCTTGCT TTCTCTCTGG TTTTATTCC ACAAAGAGCC TGGAGGTCAG AGTCTACCTG				164
CTCTATGTCC TGACACACTC TTAGCTTTAT GACCCCAAGC CTGGGAGGAA ATTTCCTGGG				224

66570334360

Year	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

[illegible]

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CGCTTATATC TATGACAAAT TCATCCCAAA GTACTTAAGT TAQAAACACA TACCTTCATA 2052
 ATATCCCTGA AAATTTTAAO AOOOAGCTTT TGTITTCOTT ATTTTTCAA AGTAAAAOAT 2112
 GTTAACTGAG ATTGTTTAAO GTCACAAAAT AAGTCAGAAAT TTTGGATTAA AACAAOAAAT 2172
 TAAATOTOTT CTTTTCAACA GTATATACTO AAAOTAAGAT OOOTCAGACT CTTTGAOTTO 2232
 ATATTTTTOT TTCTOCTTTO TAAAGOTGAA AACTGAGAGG TCAAGGAAGT TOTTCAAAAG 2292
 CACAGAGCTO GGAATTCAAC TCCAGAGCTC CACTGAGCTO ATTAGGTAGA TTTTAAATTT 2352
 TAAAAATATA GGTCAAGCTA CGTCATTCTC ACAOTCTACT CATTAGGOTT AOGAAACATT 2412
 GCATTCACTC TGGGCATGGA CAOCGAGTCT AOOOAGTCCT CAGTTTCTCA AGTTTTOCTT 2472
 TGCCTTTTTA CACCTTCACA AACACTTGAC ATTTAAATC AGTGATGCCA AACTTAAGCTO 2532
 GCAAGTGAGT GATCCTGTTG ACCCAAAACA GCTTAGGAAC CATTTCAAAT CTATAGAGTT 2592
 AAAAAOAAAA GCTCATCAGT AAGAAAATCC AATATGTTCA AGTCCCTTGA TTAAGGATOT 2652
 TATAAAATAA TTGAAATGCA ATCAAACCAA CTATTTTAACT TCCAAATTAC ACCTTTAAAA 2712
 TTCCAAAGAA AGTTCTTCTT CTATATTTCT TTGGGATTAC TAATTGCTAT TAGGACATCT 2772
 TAACTGGCAT TCATGGAAGG CTGCAGGGCA TAACATTATC CAAAAGTCAA ATGCCCCATA 2832
 GTTTTGAACT TCACAGATTA AACTGTAAAC AAAATAAAAT TAGGCATATT TACAAOCTAG 2892
 TTTCTTTCTT TCTTTTTTCT CTTTCTTCTT TTCTTTCTTT CTTTCTTCTT TTCTTTCTTT 2952
 CTTTCTTCTT TTCTCTTCTT TTCTTTCTT CTTTCTTCTT TTCTGAGCAA TTACAGACAA 3012
 ATCACTCAAG AGCTACTTCA ATAACCATAT TTTCGATTTC AG AC CGT GAT AAT 3065

Asn Arg Asp Asn
125

ACC TAC AAC COA GTO TCA GAO GAT CTO AGA AOC AGA ATT GAA GTC CTO 3113
 Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu
130 135 140

AAO CGC AAA GTC ATA GAA AAA GTA CAO CAT ATC CAO CTT CTO CAO AAA 3161
 Lys Arg Lys Val Ile Glu Lys Val Glu His Ile Glu Leu Leu Glu Lys
145 150 155

AAT GTT AGA OCT CAO TTO GTT GAT ATO AAA COA CTO GAO GTAAOTATOT 3210
 Asn Val Arg Ala Glu Leu Val Asp Met Lys Arg Leu Glu
160 165 170

GGCTGTGGTC CCGAGTGCTC TTGTTTTTGA GTAGAGGGAA AAGGAGGGCG ATAGTTATGC 3270
 ACTGAGTGTC TACTATATOC AGAAGAAAAGT GTTATATCCA TCATCTACCT AAAAAOTAGT 3330
 ATTATTTTCC TCACTCCACA GTTGAAGAAA AAAAAATTCA GAGATATTAA GTAAATTTTC 3390
 CAACGTACAT AGATAAGTAAT TCAAAAGCAAT GTTCAOTCCC TOTCTATTCC AAGCCATTAC 3450
 ATCACCACAC CTCTGAGGCC TCAAGCCTGAG TTCACCAAGG ATCATTTAAT TAGCGTTTCC 3510
 TTTGAGAGGG AATAAGCACCT TACTCTTGAAT CCATTCTGAG OCTAAGATGA ATTAACAGOC 3570
 ATCCATTGCT TATCCTGGCT AOGCCTGCAA TACCCAACAT CTCTTCCACT GAGGGTGTCTC 3630
 GATAAGCAAG AAACAGAGAA TATTAAGTGG TAGGTCTCCG AGTCAAAAAA AATGAAACCA 3690
 OTTTCCAGAA GAAAAATTAA CTACCAAGAA CTCAATAGAC GTAGTTTATG TATTTOTATC 3750
 TACATTTTCT CTTTATTTTT CTCCCCCTCTC TCTAG GTO GAC ATT GAT ATT AAG 3803

Val Asp Ile Asp Ile Lys
175

ATC COA TCT TOT COA GGO TCA TGC AGT AAG OCT TTA OCT COT GAA GTA 3851
 Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val
180 185 190

GAT CTO AAG GAC TAT GAA GAT CAO CAO AAG CAA CTT GAA CAO GTC ATT 3899

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Asp	Leu	Lys 195	Asp	Tyr	Glu	Asp	Glu 200	Glu	Lys	Glu	Leu	Glu 205	Glu	Val	Ile	
OCC	AAA	OAC	TTA	CTT	CCC	TCT	AGA	GAT	AGG	CAA	CAC	TTA	CCA	CTO	ATA	3947
Ala	Lys	Asp	Leu	Leu	Pro	Ser	Arg	Asp	Arg	Glu	His	Leu	Pro	Leu	Ile	
	210					215					220					
AAA	ATO	AAA	CCA	OTT	CCA	OAC	TTO	OTT	CCC	GOA	AAT	TTT	AAO	AOC	CAO	3995
Lys	Met	Lys	Pro	Val	Pro	Asp	Leu	Val	Pro	Gly	Asn	Phe	Lys	Ser	Glu	
225					230					235					240	
CTT	CAG	AAO	OTA	CCC	CCA	GAG	TOO	AAO	OCA	TTA	ACA	OAC	ATO	CCO	CAO	4043
Leu	Glu	Lys	Val	Pro	Pro	Glu	Trp	Lys	Ala	Leu	Thr	Asp	Met	Pro	Glu	
				245					250					255		
ATO	AOA	ATO	OAO	TTA	OAO	AOA	CCT	OOT	OGA	AAT	OAO	ATT	ACT	COA	OGA	4091
Met	Arg	Met		Leu	Glu	Arg	Pro		Gly	Asn	Glu	Ile	Thr	Arg	Gly	
			260					265					270			
OGC	TCC	ACC	TCT	TAT	OGA	ACC	OGA	TCA	GAG	ACG	GAA	AGC	CCC	AOO	AAC	4139
Gly	Ser	Thr	Ser	Tyr	Gly	Thr	Gly	Ser	Glu	Thr	Glu	Ser	Pro	Arg	Asn	
		275					280					285				
CCT	AGC	AOT	OCT	OGA	AOC	TOO	AAC	TCT	OGG	AOC	TCT	OGA	CCT	OGA	AOT	4187
Pro	Ser	Ser	Ala	Gly	Ser	Trp	Asn	Ser	Gly	Ser	Ser	Gly	Pro	Gly	Ser	
		290				295					300					
ACT	OGA	AAC	COA	AAC	CCT	OGG	AOC	TCT	OGG	ACT	OGA	OGG	ACT	GCA	ACC	4235
Thr	Gly	Asn	Arg	Asn	Pro	Gly	Ser	Ser	Gly		Gly	Gly	Thr	Ala	Thr	
305					310					315					320	
TOO	AAA	CCT	OGG	AOC	TCT	OGA	CCT	OGA	AOT	OCT	OGA	AOC	TOO	AAC	TCT	4283
Trp	Lys	Pro	Gly	Ser	Ser	Gly	Pro	Gly	Ser	Ala	Gly	Ser	Trp	Asn	Ser	
				325						330				335		
OGG	AOC	TCT	OGA	ACT	OGA	AOT	ACT	OGA	AAC	CAA	AAC	CCT	OGG	AOC	CCT	4331
Gly	Ser	Ser	Gly	Thr	Gly	Ser	Thr	Gly	Asn	Glu	Asn	Pro	Gly	Ser	Pro	
			340					345					350			
AOA	CCT	OOT	AOT	ACC	OGA	ACC	TOO	AAT	CCT	OGC	AOC	TCT	GAA	COC	OGA	4379
Arg	Pro	Gly	Ser	Thr	Gly	Thr	Trp	Asn	Pro	Gly	Ser		Glu	Arg	Gly	
		355					360					365				
AOT	OCT	OGG	CAC	TOO	ACC	TCT	OAO	AOC	TCT	OTA	TCT	OOT	AOT	ACT	OGA	4427
Ser	Ala	Gly	His	Trp	Thr	Ser	Glu	Ser	Ser	Val	Ser	Gly	Ser	Thr	Gly	
		370				375					380					
CAA	TOO	CAC	TCT	OAA	TCT	OGA	AOT	TTT	AOO	CCA	OAT	AOC	CCA	OGC	TCT	4475
Glu	Trp	His	Ser	Glu	Ser	Gly	Ser	Phe	Arg	Pro	Asp	Ser	Pro	Gly	Ser	
385					390					395					400	
OGG	AAC	OGC	AOO	CCT	AAC	AAC	CCA	OAC	TOO	OGC	ACA	TTT	GAA	OAO	OTO	4523
Gly	Asn	Ala	Arg	Pro	Asn	Asn	Pro	Asp	Trp	Gly	Thr	Phe	Glu	Glu	Val	
				405					410					415		
TCA	OGA	AAT	OTA	AOT	CCA	OGG	ACA	AOO	AOA	OAO	TAC	CAC	ACA	OAA	AAA	4571
Ser	Gly	Asn	Val	Ser	Pro	Gly	Thr	Arg	Arg	Glu	Tyr	His	Thr	Glu	Lys	
			420					425					430			
CTO	OTC	ACT	TCT	AAA	OGA	OAT	AAA	OAO	CTC	AOO	ACT	OOT	AAA	OAO	AAO	4619
Leu	Val	Thr	Ser	Lys	Gly	Asp	Lys	Glu	Leu	Arg	Thr	Gly	Lys	Glu	Lys	
		435					440					445				
OTC	ACC	TCT	OOT	AOC	ACA	ACC	ACC	ACO	COT	COT	TCA	TOC	TCT	AAA	ACC	4667
Val	Thr	Ser	Gly	Ser	Thr	Thr	Thr	Thr	Arg	Arg	Ser	Cys	Ser	Lys	Thr	
		450				455					460					
OTT	ACT	AAO	ACT	OTT	ATT	OOT	CCT	OAT	OOT	CAC	AAA	GAA	OTT	ACC	AAA	4715
Val	Thr	Lys	Thr	Val	Ile	Gly	Pro	Asp	Gly	His	Lys	Glu	Val	Thr	Lys	
465					470					475					480	
OAA	OTO	OTO	ACC	TCC	OAA	OAT	OOT	TCT	OAC	TOT	CCC	OAO	GCA	ATO	OAT	4763
Glu	Val	Val	Thr	Ser	Glu	Asp	Gly	Ser	Asp	Cys	Pro	Glu	Ala	Met	Asp	
				485					490					495		
TTA	OGC	ACA	TTG	TCT	OGC	ATA	OOT	ACT	CTG	OAT	OGG	TTT	COC	CAT	AOO	4811
Leu	Gly	Thr	Leu	Ser	Gly	Ile	Gly	Thr	Leu	Asp	Gly	Phe	Arg	His	Arg	
			500					505					510			
CAC	CCT	OAT	OAA	OCT	GCC	TTC	TTC	OAC	ACT	OGC	TCA	ACT	OGA	AAA	ACA	4859

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His	Pro	Asp	Glu	Ala	Ala	Phe	Phe	Asp	Thr	Ala	Ser	Thr	Gly	Lys	Thr	
		515					520					525				
TTC	CCA	GGT	TTC	TTC	TCA	CCT	ATG	TTA	GGA	GAG	TTT	GTC	AGT	GAG	ACT	4907
Phe	Pro	Gly	Phe	Phe	Ser	Pro	Met	Leu	Gly	Glu	Phe	Val	Ser	Glu	Thr	
	530					535					540					
GAG	TCT	AGG	GGC	TCA	GAA	TCT	GGC	ATC	TTC	ACA	AAT	ACA	AAG	GAA	TCC	4955
Glu	Ser	Arg	Gly	Ser	Glu	Ser	Gly	Ile	Phe	Thr	Asn	Thr	Lys	Glu	Ser	
545					550				555					560		
AGT	TCT	CAT	CAC	CCT	GGG	ATA	GCT	GAA	TTC	CCT	TCC	CGT	GGT	AAA	TCT	5003
Ser	Ser	His	His	Pro	Gly	Ile	Ala	Glu	Phe	Pro	Ser	Arg	Gly	Lys	Ser	
				565					570					575		
TCA	AGT	TAC	AGC	AAA	CAA	TTT	ACT	AGT	AGC	ACG	AGT	TAC	AAC	AGA	GGA	5051
Ser	Ser	Tyr	Ser	Lys	Gln	Phe	Thr	Ser	Ser	Thr	Ser	Tyr	Asn	Arg	Gly	
			580					585					590			
GAC	TCC	ACA	TTT	GAA	AGC	AAG	AGC	TAT	AAA	ATG	GCA	GAT	GAG	GCC	GGA	5099
Asp	Ser	Thr	Phe	Glu	Ser	Lys	Ser	Tyr	Lys	Met	Ala	Asp	Glu	Ala	Gly	
	595						600					605				
AGT	GAA	GCC	GAT	CAT	GAA	GGA	ACA	CAT	AGC	ACC	AAG	AGA	GGC	CAT	GCT	5147
Ser	Glu	Ala	Asp	His	Glu	Gly	Thr	His	Ser	Thr	Lys	Arg	Gly	His	Ala	
	610					615					620					
AAA	TCT	CGC	CCT	GTC	AGA	GGT	ATC	CAC	ACT	TCT	CCT	TTG	GGG	AAG	CCT	5195
Lys	Ser	Arg	Pro	Val	Arg	Gly	Ile	His	Thr	Ser	Pro	Leu	Gly	Lys	Pro	
625					630					635				640		
TCC	CTG	TCC	CCC	TAG	ACT	AAAT	TATTC	TGC	ACAT	TGT	TCCC	ATGCC				5247
Ser	Leu	Ser	Pro			645										
CCTTGCATTT	CCTTCTTAAC	TCTCTOTTAC	ACGTCAATGA	AACTACACTT	TTTTGGTCTG											5307
TTTTTGTGCT	AGACTGTAAO	TTCTTTGGGG	GCAAGGCGCTT	TGTCTGTCTC	ATCTCTGTAT											5367
TCCCAAATOC	CTAACAGTAC	AGAAGCCATGA	CTCAATAAAT	ACATGTTAAA	TGGATGAATO											5427
AATTCCTCTG	AAACTCTATT	TGAGCTTATT	TAOTCAAATT	CTTTCACAT	TCAAAGTOTO											5487
TGCTATTAGA	ATTGTCACCC	AACTGATTAA	TCACATTTTT	AGTATGTGTC	TCAAGTTOACA											5547
TTTAAGTCAO	GCTAAATACA	AGTTGTGTTA	GTATTAAOTG	AGCTTAGCTA	CCTGTACTOG											5607
TTACTTGOCTA	TTAGTTTGTG	CAAGTAAAAAT	TCCAAATACA	TTTGAAGAAA	ATCCCTTTTO											5667
CAATTTGTAG	GTATAAATAA	CCGCTTATTT	GCATAAGTTC	TATCCCACTG	TAAGTGCATC											5727
CTTTCCTTAT	GAAGGGAAGG	AAAGGAAGAA	GAAAGAAAGG	AAAGGAAAGA	AACAATATTT											5787
GCCTTATTTA	ATCTGAAGCCG	TGCCTATCTT	TGTAAAGTTA	AATGAGAATA	ACTTCTTCCA											5847
ACCAAGCTTAA	TTTTTTTTTT	AGACTGTGAT	GATGTCCTCC	AAACACATCC	TTCAAGTACC											5907
CAAAATGACA	TTTTCAATAT	CAAAGTATCC	GAATCC													5943

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Ser Met Arg Ile Val Cys Leu Val Leu Ser Val Val Gly Thr
 1 5 10 15
 Ala Trp Thr Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly
 20 25 30
 Gly Val Arg Gly Pro Arg Val Val Glu Arg His Glu Ser Ala Cys Lys
 35 40 45

644
 544
 444
 344
 244
 144
 44
 4
 1

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Asp	Ser	Asp	Trp	Pro	Phe	Cys	Ser	Asp	Glu	Asp	Trp	Asa	Tyr	Lys	Cys
50						55					60				
Pro	Ser	Gly	Cys	Arg	Met	Lys	Gly	Leu	Ile	Asp	Glu	Val	Asa	Gln	Asp
65					70					75					80
Phe	Thr	Asa	Arg	Ile	Asa	Lys	Leu	Lys	Asa	Ser	Leu	Phe	Glu	Tyr	Gln
			85						90					95	
Lys	Asa	Asa	Lys	Asp	Ser	His	Ser	Leu	Thr	Thr	Asa	Ile	Met	Glu	Ile
			100					105					110		
Leu	Arg	Gly	Asp	Phe	Ser	Ser	Ala	Asa	Asa	Arg	Asp	Asa	Thr	Tyr	Asa
		115					120					125			
Arg	Val	Ser	Glu	Asp	Leu	Arg	Ser	Arg	Ile	Glu	Val	Leu	Lys	Arg	Lys
	130					135					140				
Val	Ile	Glu	Lys	Val	Gln	His	Ile	Gln	Leu	Leu	Gln	Lys	Asa	Val	Arg
145					150					155					160
Ala	Gln	Leu	Val	Asp	Met	Lys	Arg	Leu	Glu	Val	Asp	Ile	Asp	Ile	Lys
			165						170					175	
Ile	Arg	Ser	Cys	Arg	Gly	Ser	Cys	Ser	Arg	Ala	Leu	Ala	Arg	Glu	Val
			180					185					190		
Asp	Leu	Lys	Asp	Tyr	Glu	Asp	Gln	Gln	Lys	Gln	Leu	Gln	Gln	Val	Ile
	195						200					205			
Ala	Lys	Asp	Leu	Leu	Pro	Ser	Arg	Asp	Arg	Gln	His	Leu	Pro	Leu	Ile
	210					215					220				
Lys	Met	Lys	Pro	Val	Pro	Asp	Leu	Val	Pro	Gly	Asa	Phe	Lys	Ser	Gln
225					230					235					240
Leu	Gln	Lys	Val	Pro	Pro	Glu	Trp	Lys	Ala	Leu	Thr	Asp	Met	Pro	Gln
			245						250					255	
Met	Arg	Met	Glu	Leu	Glu	Arg	Pro	Gly	Gly	Asa	Glu	Ile	Thr	Arg	Gly
		260						265					270		
Gly	Ser	Thr	Ser	Tyr	Gly	Thr	Gly	Ser	Glu	Thr	Glu	Ser	Pro	Arg	Asa
		275					280					285			
Pro	Ser	Ser	Ala	Gly	Ser	Trp	Asa	Ser	Gly	Ser	Ser	Gly	Pro	Gly	Ser
	290					295					300				
Thr	Gly	Asa	Arg	Asa	Pro	Gly	Ser	Ser	Gly	Thr	Gly	Gly	Thr	Ala	Thr
305					310					315					320
Trp	Lys	Pro	Gly	Ser	Ser	Gly	Pro	Gly	Ser	Ala	Gly	Ser	Trp	Asa	Ser
			325						330					335	
Gly	Ser	Ser	Gly	Thr	Gly	Ser	Thr	Gly	Asa	Gln	Asa	Pro	Gly	Ser	Pro
			340					345					350		
Arg	Pro	Gly	Ser	Thr	Gly	Thr	Trp	Asa	Pro	Gly	Ser	Ser	Glu	Arg	Gly
		355					360					365			
Ser	Ala	Gly	His	Trp	Thr	Ser	Glu	Ser	Ser	Val	Ser	Gly	Ser	Thr	Gly
	370					375					380				
Gln	Trp	His	Ser	Gln	Ser	Gly	Ser	Phe	Arg	Pro	Asp	Ser	Pro	Gly	Ser
385					390					395					400
Gly	Asa	Ala	Arg	Pro	Asa	Asa	Pro	Asp	Trp	Gly	Thr	Phe	Gln	Gln	Val
			405						410					415	
Ser	Gly	Asa	Val	Ser	Pro	Gly	Thr	Arg	Arg	Glu	Tyr	His	Thr	Gln	Lys
			420					425					430		
Leu	Val	Thr	Ser	Lys	Gly	Asp	Lys	Glu	Leu	Arg	Thr	Gly	Lys	Gln	Lys
		435					440					445			
Val	Thr	Ser	Gly	Ser	Thr	Thr	Thr	Thr	Arg	Arg	Ser	Cys	Ser	Lys	Thr
	450					455					460				
Val	Thr	Lys	Thr	Val	Ile	Gly	Pro	Asp	Gly	His	Lys	Gln	Val	Thr	Lys
465					470					475					480

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Glu Val Val Thr Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp
 485 490 495
 Leu Gly Thr Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg
 500 505 510
 His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr
 515 520 525
 Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr
 530 535 540
 Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu Ser
 545 550 555 560
 Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly Lys Ser
 565 570 575
 Ser Ser Tyr Ser Lys Glu Phe Thr Ser Ser Thr Ser Tyr Asn Arg Gly
 580 585 590
 Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala Asp Glu Ala Gly
 595 600 605
 Ser Glu Ala Asp His Glu Gly Thr His Ser Thr Lys Arg Gly His Ala
 610 615 620
 Lys Ser Arg Pro Val Arg Gly Ile His Thr Ser Pro Leu Gly Lys Pro
 625 630 635 640
 Ser Leu Ser Pro

(2) INFORMATION FOR SEQ ID NO3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6878 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: human Striagen B-beta chain

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 1..469

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 470..583

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 584..627

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 628..649

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 650..693

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 694..712

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 713..802

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 803..870

(ix) FEATURE:

(A) NAME/KEY: intron
(B) LOCATION: 5271..5830

(i x) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 5831..5944

(i x) FEATURE:
(A) NAME/KEY: intron
(B) LOCATION: 5945..6632

(i x) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 6633..6758

(i x) FEATURE:
(A) NAME/KEY: intron
(B) LOCATION: 6759..6966

(i x) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 6967..7252

(i x) FEATURE:
(A) NAME/KEY: intron
(B) LOCATION: 7253..7870

(i x) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 7871..8102

(i x) FEATURE:
(A) NAME/KEY: 3'UTR
(B) LOCATION: 8103..8537

(i x) FEATURE:
(A) NAME/KEY: misc_RNA
(B) LOCATION: 8538..8878

(i x) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: join(470..583, 3258..3449, 3939..4122, 5043..5270, 5831..5944, 6633..6758, 6967..7252, 7871..8102)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCATGC	CCCTTTTGA	ATAGACTTAT	GTCAATTGTCA	GAAAAACATAA	GCATTTTATGG	60
TATATCATT	ATGATCAGC	ATTTTAGTGG	TTGCTTGTG	AGTAGGTCAA	ATTTACTAA	120
CTTAGATTTG	TTTTCTCACA	TATTCCTTCG	GAAGCTTGTGT	AATTTCCACA	TTAATTTACC	180
AGAAACAAAG	TACACACTCT	CTTTGAAGAG	TGCCCTAACT	TCCCATCATT	TTGTCCAATT	240
AAATGAATTG	AAGAAATTTA	ATGTTTCTAA	ACTAGACCAA	CAAAAGAAATA	TAATTTGTATG	300
ACAAATAAAT	AAAGCTTTGCT	GGGAAAGATGT	TGCTTAAATG	ATAAAAATGTT	TCAAGCCAACA	360
AGTGAACCAA	AAATTAAATA	TTAACTAAAG	AAAAGGTAAAC	ATTTCTGAAG	TCATTCCTAG	420
CAGAGGACTC	AGATATATAT	AGGATTTAAG	ATCTCTCAAT	TAAATCTAC	ATG AAA	475
Met Lys						
1						
AGG ATG GTT TCT TGG ACG TTC CAC AAA CTT AAA ACC ATG AAA CAT CTA	523					
Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys His Leu						
5 10 15						
TTA TTG CTA CTA TTG TGT GTT TTT CTA GTT AAG TCC CAA GGT GTC AAC	571					
Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly Val Asn						
20 25 30						
GAC AAT GAG GAG GTGAATTTTT TAAAGCATT	623					
Asp Asn Gln Gln						
35						
TTAATATAAG ATGTAACATA ATCATATTAT GTGCTTATTT TAATGAAATT AGCATTGCTT	683					

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ATAOTTATOA	AATGGAATTO	TAAACCTCTO	ACTTATTOTA	TTTAAAGAAAT	OTTTTCATAOT	743
ATTTCTTATA	TAAAAACAAA	OTAATTTCTT	OTTTTCTAOT	TTATCACCTT	TOTTTTCTTA	803
AGATGAAGAT	OGCTTAOCTA	ATOTAAOATG	TOTTTTTCTC	ACTTUCTATT	CTOAGTACTO	863
TOATTTTCAT	TTACTTCTAO	CAATACAOGA	TTACAATTAA	GAOGACAAGA	TCTGAAAAATC	923
TCACAAACTA	TAAAAATAA	AAAGAOCAGA	ATTTTAAOAT	AAAAOAAACT	OGTGOATAOOT	983
AGATTOTICT	TTGOTGAAGG	AAOGTAATAT	ATATTOTTAC	TOAGATTACT	ATTTATAAAA	1043
ATTATAACTA	AGCCTAAAAO	CAAAATACAT	CAAGTOTAAT	GATAGAAAAAT	GAATATTTOC	1103
TTTTTTCAGA	TOAAAAOITC	AAATTAGAOI	TAOTOTOTAT	TOTTATTATT	AATAOTTATO	1163
AAACACOGTT	CAOTCTAATT	TATTTATITG	TAGAACAOIT	TOTCCTCAAC	TATTATTTTT	1223
OGTOACTTAT	TGCTOTTAAT	TTOCAOTTAC	TAAAAATACA	GAATTOCATT	TAGGACAATO	1283
GATATTTAAO	AAATTTAAAT	TTTATCATCA	AACOTATCAT	OGCCAAATTT	CTTACATATA	1343
GCATAOTATC	ATTAAACTAG	AAATAAGAAI	ACACAATAAT	ATTTAAATOA	AGTGAATTCAT	1403
TTGOGATCAT	TATTGAOTTT	CAAGOGAACT	TOAGTGTITG	ACTTATCAGA	CTCTACATOT	1463
AAGAACATAT	AGTTAATCTO	OTTOTOTOTO	TAAAAACATA	TGOTTAATCT	OGTTAAOTCT	1523
OGTTAATCAT	ATTAOGTAAG	AAAAATOTAA	AGAAOTOTTA	AGACGAAAT	TTTGTAAAGT	1583
ACTCTOCAAA	OCACITTCAC	ATTTCTOCTT	ATCAACTAAA	CCTCACAGAG	ATAOTTTAAT	1643
AGTTTAOOC	TTAAAAOTGA	TTTTGATTAT	TCAACAAOTG	OGCTTCATAA	TTTCTTTAAO	1703
TGTTTTTCTT	TAAOTATATA	CTTTCTTTAA	ATATTTTTTA	AAATTTCTTT	TTCTCTAOTA	1763
AAOGCAGACC	ATCCATGCTA	CCTCTCTAOT	OGCACTCTGA	AATAAAAAOA	AAATAOTTTT	1823
CTCTOTTATA	ATTOTATITG	TAATAAGCAO	ATGAATCACA	TTTCTTAAAA	TTTOTTITAG	1883
AGAGOGTAAG	CTCTOACTAG	OGCCATGACT	TCAATOTGAA	ATATOTATAT	ATCCTCCGAA	1943
TCITTTACATA	TTAAGAAOTG	ATATAOTCAA	CTOOTTAAAC	AGGAAAAATCT	OGAACAOCC	2003
OGCTOGOTTT	TAACTTTAOC	ACCATCCTAC	TAAATOTTAA	ATAATATTAT	AATCTAATOA	2063
ATAAATOACA	ATOCAATTCC	AAATAGAOIT	CATCTOATOA	CTTCTAGACT	CACAAAAATTO	2123
CAAGAGAGCT	CAOTTOTITG	TCAOTTOTIT	CAAAATCATOT	COTTTOTTTA	TTTGTAAATTA	2183
AOCTCCAAA	GATGTATAOC	TACTOACAAA	AAAAAAAATG	AGAAOTOTAOT	TAATCCAAAT	2243
CAAAACTTTT	CTATTGCAAT	OGOTATTTTC	TGCTTCATTA	TCCTTTAATA	TAATATTTTA	2303
AGTTAOCAG	TAATTTTAAT	TACAATOCAC	AAOGCTTGAO	AATTATTTTA	AATATAAGAA	2363
AATCATAATG	TTTGAATAAG	AAATCATGTA	AGAAATTTCA	AGATAATGOT	TTAACAAATA	2423
ATTTTOTTGA	TAGAAAGATA	OGCTAAAAOT	GAATTTGAAA	OTGGAAGAGG	CACTTAAACT	2483
GTAGTACTIT	TTATOTOTGA	TTCCAOTAAA	AATAOTAATG	AGCACTTATT	ATTGCCAAGT	2543
ACTGTTCTGA	OGGTACCATA	TOCAATAAOT	TATTTAATCC	TTACAATAAT	CTTGTAAOGC	2603
AGATTCAAA	TATCATTACA	CTTATTTTAC	AGATGAGAAA	ACTGOGGOCAC	AGATAAAOCA	2663
ACTTOCCCAA	OGTCTCATAG	CTGTAAOTCA	ACCCATACOT	CAAGACCTAC	AAOTAGCCGA	2723
OGTCCAGAGT	ACATTATGAG	OGTCAAAOAT	TGTCTTATTA	CAAAATAAAT	CCAAOTAGAA	2783
TCAACCTTTA	ATAAGTCTTT	AAOTGTCTCT	AAATATOTTT	ATATAOGAOT	CTAATCACCA	2843
ATTACAAAA	ATGAAAOTAG	OGAAATGATT	AACAATAATC	ATAGGAATCT	AACAATCCAA	2903
GTGCTTGAO	AATATTCAAT	CTTCTTOACA	GTATAGATTG	TTTACAATTT	COTAAOTTCC	2963
AATGTATGTT	TTAGGAATAT	GAOGTCATTA	CTATTCATAA	TCTOATACAG	CTTTATCCTA	3023
AGOGCTCTCT	TTAAAAACTA	CACTOCATCA	TAGCTTTTTT	GTGCAOTTGO	TCTTTCTACT	3083

05570-334220

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OTTACTGAAC	AOTAAOCAAC	CTACAQATTC	ACTATCACCA	ACCAOCCAOT	TOATOGATCT	3143
TAAOCAAAAT	ATCAAOCCTG	TOATAACCTA	AATTATAAAA	TGAOOGOTTT	OGAATAOTTA	3203
CATTCCAAAT	CTTCTATAAC	ACTCTGTATT	ATATTTCTOC	CTCATTCCCT	GTAG OGT	3260
					Gly	
TTC TTC AOT OCC COT OGT CAT COA CCC CTT GAC AAO AAO AGA GAA GAO	3308					
Phe Phe Ser Ala Arg Gly His Arg Pro Leu Asp Lys Lys Arg Glu Glu						
40 45 50 55						
OGT CCC AOC CTO AOO CCT OCC CCA CCO CCC ATC AOT OGA OGT OGC TAT	3356					
Ala Pro Ser Leu Arg Pro Ala Pro Pro Pro Ile Ser Gly Gly Gly Tyr						
60 65 70						
COG OCT COT CCA OCC AAA OCA OCT OCC ACT CAA AAO AAA GTA GAA AOA	3404					
Arg Ala Arg Pro Ala Lys Ala Ala Ala Thr Glu Lys Lys Val Glu Arg						
75 80 85						
AAA OCC CCT GAT OCT OGA OGC TGT CTT CAC OCT GAC CCA GAC CTO	3449					
Lys Ala Pro Asp Ala Gly Gly Cys Leu His Ala Asp Pro Asp Leu						
90 95 100						
GTGGGTGCAC	TOATGTTTCT	TOCAGTGGTG	GTCTCTCAT	GCAGAGAAA	CCTGTAOTCA	3509
TGGCAGTCTG	CTAATGTTTC	ACTGACCCAC	ATTACCATCA	CTGTTATTTT	GTGTTGTTAT	3569
TTTGGAAATA	AAATTCAAAA	CATAAACATA	TTGGGCCTTT	GGTTTAAGCT	TTCTTTCTTG	3629
TTTTCTTTGG	TCTGGGCCCA	AAATTTCAAA	TTAGGATATG	TGGGTGCCAC	CTTTCCATTT	3689
GTATTTTGGC	ACTGCCITTT	TTTAGTTGGT	AAAATTTTCA	TAGCCCAATT	ATATTTTTTC	3749
TGGGTTAAOT	AATATTTTAA	ATCTCTATGA	GAOTATGATG	ATGACTTTTC	AATTTCTGOT	3809
CTTACAQAAA	ACCAAATAAT	AAATTTTTAT	GTGGCTAAT	CGTATCGCTG	AATTTTCCTA	3869
TGTGCTATTT	TAACAAATGT	CCATGACCCA	AATCCTTCAT	CTAATGCCTG	CTATTTTCTT	3929
TOTTTTTTAA	GGG GTG TTO	TGT CCT ACA	GGA TGT CAG	TTO CAA GAG	OCT	3977
	Gly Val Leu Cys Pro Thr Gly Cys Glu Leu Glu Glu Ala					
	105 110 115					
TTO CTA CAA CAG GAA AOO CCA ATC AGA AAT AOT GTT GAT GAG TTA AAT	4025					
Leu Leu Glu Glu Glu Arg Pro Ile Arg Asn Ser Val Asp Glu Leu Asn						
120 125 130						
AAC AAT OTG GAA OCT GTT TCC CAG ACC TCC TCT TCT TCC TTT CAG TAC	4073					
Asn Asn Val Glu Ala Val Ser Glu Thr Ser Ser Ser Ser Phe Glu Tyr						
135 140 145						
ATG TAT TTO CTO AAA GAC CTO TGG CAA AAG AOO CAG AAG CAA GTA AAA	4122					
Met Tyr Leu Leu Lys Asp Leu Trp Glu Lys Arg Glu Lys Glu Val Lys						
150 155 160						
GTAGATATCC	TTTGTCTTTC	CATTGCAATT	TCAOCTATAA	AATTGGAACC	GTAGACTOC	4182
CACGAGAATO	CATGGTTTGT	AGAAAGATTAA	CATTTCTGGG	TTAGTGAATA	GCATTCATAC	4242
OGTTTTGGGC	ACCTTCCCTT	GCAACTTGGC	AGATAAGCAC	TATTCAGCTC	TTATTTCCCAO	4302
TCTGACATCA	GCAGGTGTGA	TTTTCTATGA	AAAATTCTAC	TATGACTCCT	TATTTTAAOT	4362
ATACAAGAAA	CTTGTGACTC	AGAAAGATAAT	ATTTACAGAG	TGAAAAAAA	CCCCTAGCAT	4422
TTATAOTTTT	AACATTTTGA	GTTTTGAATG	AGAGAGTTAT	CCATAATATA	TTCAATTOTO	4482
TTGTGGATAA	TOACACCTAA	CCTGTGAATC	TTGAAGTCAG	AATOTTGAGT	GCTOTTGACT	4542
TGGTGGTCAG	GAACACGCTA	GTGCGTGAOC	CTGGCACAGG	CATCTCAOTG	AGTAOCATAC	4602
CCACAGTTGG	AAATTTTTTC	AGAAATCAA	AGGAATCATG	ACATCTTATA	AATTTCAAAG	4662
TTCTGCTATA	CTTATGTGAA	ATGGAATAAA	AAATCAAACA	TATCCACTCT	GTAAOATTGA	4722
ACTTCTCAGA	TGAAAGACCC	CAATACTGCT	TTCTCCTCTT	TTCCCTCACC	AAAGAAATAA	4782
ACAACCTATT	TCATTTATTA	CTGACACAAA	TCTTTAGCGT	ATACCTATGG	TAAATTACTA	4842

GCTTQ = 0072260

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GTATGTTGTT TAGGATTTAT GTTAATTTGT ATATGTCATG CCCCCAATCA TTTCCTACTAA	4902
ATATGACTAT ATATCATAAC TGCTTGGTGA TAGCTCAATG TTTAATAATT TATTCTCAGA	4962
AAATCAAAAT TGTATAATTA AATACATTAG TTTTATGAGG CAAAAATGCT AACTATTTCT	5022
ACATAATTTT ATTTTTCAG AT AAT GAA AAT GTA GTC AAT GAG TAC TCC	5071
Asp Asn Glu Asn Val Val Asn Glu Tyr Ser 165 170	
TCA GAA CTG GAA AAG CAC CAA TTA TAT ATA GAT GAG ACT GTG AAT AGC	5119
Ser Glu Leu Glu Lys His Glu Leu Tyr Ile Asp Glu Thr Val Asn Ser	175 180 185
AAT ATC CCA ACT AAC CTT CGT GTG CTT CGT TCA ATC CTG GAA AAC CTG	5167
Asn Ile Pro Thr Asn Leu Arg Val Leu Arg Ser Ile Leu Glu Asn Leu	190 195 200 205
AGA AGC AAA ATA CAA AAG TTA GAA TCT GAT GTC TCA OCT CAA ATG GAA	5215
Arg Ser Lys Ile Glu Lys Leu Glu Ser Asp Val Ser Ala Glu Met Glu	210 215 220
TAT TGT CGC ACC CCA TGC ACT GTC AGT TGC AAT ATT CCT GTG GTG TCT	5263
Tyr Cys Arg Thr Pro Cys Thr Val Ser Cys Asn Ile Pro Val Val Ser	225 230 235
GGC AAA G GTAAGTATT CATAAACATA TTTTATGAGA GTTCCAGAGG AACTCACACA	5320
Gly Lys CCAAAAATAA GAGAACAAACA ACAACAACAA AAATGCTAAG TGGATTTTCC CAACAGATCA	5380
TAATGACATT ACAATACATC ATAAAAATAT CCTTAAGCAO TTGTGTTTTG GACTGGCCTG	5440
GTGCATTTTC TGGTTTTGAT GAGCAAGGAT GGGCACAGGT AGTCCCAAGG GTGGCTGATG	5500
TGTGCATCTG CGTACTGGCT TGAACAGATG GCAGAACCCAC AGATAAGATGT AGAAGTTTCT	5560
CCATTTTGTG TTTTCTGGGA GCTCATGGAT ATTCCAAGGAC ACAAAAAGGTG GAGAAAGAGCT	5620
TTGTTTCATCC TCTTAAGAGA TAAACGTCCT CAAAAGTGGG TTGGACTTAC TAAAGTAAAA	5680
TGAAAAATCTA ATATTTGTTA TATTATTTTC AAAAGTCTAT AATAACACAC TCCTTAATTA	5740
CTTATGTAAT GTTATTTTAA AGAATTTGTTG ACTAAATACA AAGTAATTAT GTCATAAACC	5800
CCTGAACATA ATGTTGTCTT ACATTTGCAO AA TOT GAG GAA ATT ATC AGG AAA	5853
Glu Cys Glu Glu Ile Ile Arg Lys 240 245	
GGA GGT GAA ACA TCT GAA ATG TAT CTC ATT CAA CCT GAC AGT TCT GTC	5901
Gly Gly Glu Thr Ser Glu Met Tyr Leu Ile Glu Pro Asp Ser Ser Val	250 255 260
AAA CCG TAT AGA GTA TAC TGT GAC ATG AAT ACA GAA AAT GGA G	5944
Lys Pro Tyr Arg Val Tyr Cys Asp Met Asn Thr Glu Asn Gly	265 270 275
GTAAAGCTTC GACAGTTGTT GACCTGTTGA TCTGTAATTA TTTGATACC GTAAAAATGCC	6004
AGGAAACAAO OCCAGGTGTG GTGGCTCATA CCTGTAATTC CAACACCTTG GAGAGCCAAA	6064
GTGGGCTGAT AGCTTGAAGC TAGGAGTTTG AAACTAAGCT GGGCAACATA ATGAGACCCT	6124
AACTCTACAA AAAAAAAAAA AATACCAAAA AAAAAAAAAA AATCAAGCTGT GTTGGTATGA	6184
TGTGCTGTA GTCCCAAGTA TCCAAGGAGG TAGGATGGGA GATCACCTGA GGGCACAACC	6244
TGGAGTCTTG ATCATGCTAC TGAAGTGTAG CCTGGGCAAC AGAGGATAGT GAGATCCTGT	6304
CTCAAAAAAAAA AAAAAATTAAT AAAAAAGCAO GAAACAAAGAC TTAAGTCTAA CATCTAACAT	6364
AGCTGACAAA GGAATTAATT GATGTGGAAT TCAACCTGAT ATTTAAAAAT TATAAAATAT	6424
CTATAATICA CAATTTGGGG TAAAGATAAG CACTTGCAGT TTCCAAAGAT TTTACAAATT	6484
TACCTCTCAT ATTTATTTCC TTATTGTGTC TATTTTAGAG CACCAAAATAT ATACTAAATG	6544
GAATGACAG GGAATTCAGA TATTATTTTC AAAAGTACAT TATTTGCTGT TGGTAAATAT	6604

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ATGCTCTTTT TGTTCCTGTC AACCAAAAG	GA TGG ACA GTG ATT CAO AAC CGT	6655
Gly Trp Thr Val Ile Glu Asn Arg 280 285		
CAA GAC GGT AGT GTT GAC TTT GGC AAG AAA TGG GAT CCA TAT AAA CAO	6703	
Glu Asp Gly Ser Val Asp Phe Gly Arg Lys Trp Asp Pro Tyr Lys Glu	290 295 300	
GGA TTT GGA AAT GTT GCA ACC AAC ACA GAT GGG AAG AAT TAC TOT GGC	6751	
Gly Phe Gly Asn Val Ala Thr Asn Thr Asp Gly Lys Asn Tyr Cys Gly	305 310 315	
CTA CCA G GTAACGAACA GGCATOCAAA ATAAAAATCAT TCTATTTGAA ATGGGATTTT	6808	
Leu Pro		
TTTTAATTAA AAAACATTCA TTGTTGGAAAG CCTGTTTTAG GCAGTTAAGA GGAATTTTCT	6868	
GACAAAAAATG TGGAAAGCTAA AGATAAAGGGA AGAAAAAGCAG TTTTATGTTT CCCAAAAATTT	6928	
TATTTTTGOT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT	6980	
Gly Glu Tyr Trp Leu 320		
GGA AAT GAT AAA ATT AGC CAG CTT ACC AAG ATG GGA CCC ACA GAA CTT	7028	
Gly Asn Asp Lys Ile Ser Glu Leu Thr Arg Met Gly Pro Thr Glu Leu	325 330 335 340	
TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT	7076	
Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr	345 350 355	
GGA GGA TTC ACT GTA CAG AAT GAA OCC AAC AAA TAC CAG ATC TCA GTG	7124	
Gly Gly Phe Thr Val Glu Asn Glu Ala Asn Lys Tyr Glu Ile Ser Val	360 365 370	
AAC AAA TAC AGA GGA ACA OCC GGT AAT OCC CTC ATG GAT GGA GCA TCT	7172	
Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met Asp Gly Ala Ser	375 380 385	
CAG CTG ATG GGA GAA AAC AAG ACC ATG ACC ATT CAC AAC GGC ATG TTC	7220	
Glu Leu Met Gly Glu Asn Arg Thr Met Thr Ile His Asn Gly Met Phe	390 395 400	
TTC AGC ACG TAT GAC AGA GAC AAT GAC GGC TG GTATGTGTGG	7262	
Phe Ser Thr Tyr Asp Arg Asp Asn Asp Gly Trp	405 410 415	
CACCTTTTGC TCCTGCTTTA AAAATCACAC TAATATCATT ACTCAGAAATC ATTAACAATA	7322	
TTTTTAATAAG CTACCACTTC CTGGGCACTT ACTGTCAAGCC ACTGTCTTAA GCTCTTTATG	7382	
CATCACTCGA AAGCATTTC ACTATAAAGT AGACATTCTT ATTCTCATTT TACAGATGAG	7442	
ATTTAAGAGAG ATTACGTGAT TTGTCCAATG TCACACAACCT ACCCAGAGAT AAAACTAGAA	7502	
TTTGAAGCACA GTTACTTTCT GAATAATGAG CATTTAAGATA AATACCTATA TCTCTATATT	7562	
CTAAAGTGOTO TGTGAAAACCT TTCATTTTCA TTTCAGGOT TCTCTGATAC TAAGGOTTGT	7622	
AAAAAGCTATT ATTCCAATAT AAAATAACAA ACACAATCCC TAGATGGATT GCCACAAAGG	7682	
CCCAATTATC TCTCTTTCTT GCTATAAGGAC ACAAGGAGGTC TTTGGTGTAT TAGTGTGACT	7742	
CTATGTATAG CACCCAAAGG AAAAGACTACT GTGCACACGA GTGTAAGCAGT CTTTTATGGG	7802	
TAATCTGCAA AACGTAACTT GACCACCOTA GTTCTGTTTC TAATAACGCC AAACACATTT	7862	
TCTTTCAAG G TTA ACA TCA GAT CCC AGA AAA CAG TOT TCT AAA GAA GAC	7910	
Leu Thr Ser Asp Pro Arg Lys Glu Cys Ser Lys Glu Asp 420 425		
GGT GGT GGA TGG TGG TAT AAT AGA TOT CAT GCA GCC AAT CCA AAC GGC	7958	
Gly Gly Gly Trp Trp Tyr Asn Arg Cys His Ala Asn Pro Asn Gly	430 435 440	
AGA TAC TAC TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC	8006	
Arg Tyr Tyr Trp Gly Gly Glu Tyr Thr Trp Asp Met Ala Lys His Gly		

GCTCTTTT

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445	450	455	460	
ACA GAT GAT GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA				8054
Thr Asp Asp Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser	465	470	475	
ATG AAG AAG ATG AAT ATG AAG ATC AAG CCC TTC TTC CCA CAG CAA TAGTCCCC				8109
Met Arg Lys Met Ser Met Lys Ile Arg Pro Phe Phe Pro Glu Glu	480	485	490	
TACGTAGATT TTTGCTCTTC TGTATGTGAC AACATTTTTO TACATTATGT TATTOGAATT				8169
TTCTTTTCATA CATTATATTC CTCTAAAACT CTCAGGCAGA CGTGAATGTG ACTTTTGGAA				8229
AAAAGTATAG GATAAATTAC ATTAAAAATAG CACATGATTT TCTTTTGTIT TCTTCATTTT				8289
TCTTGCTCAC CCAAGAAATA ACAAAGATAT AATTTTGAACA GAATTOGTGT TCATAATTTT				8349
AGTTCTAGTT GATTGCGAGA ATTTTCAAAT AAGGAAGAGG GGTCTTTTAT CCTTGTCTGA				8409
GGAAAACCAT GACGGAAAGG AAAAAGTGTAT GTTTAAAAAT CCACTTTTAA AACTATATTT				8469
ATTTATGTAG GATCTGTCAA AAAAAAGTTC CAAAAAGATT TATTAATTAA ACCAGACTCT				8529
GTTCGAATAA GTTAATGTTT TCTTGTTTTG TAATCCACAC ATTCAATGAG TTAGGCTTTO				8589
CACTTGTAAO GAAAGAGAGG CGTTCACAAC CTCAAATAAG TAATAAACCG GTCTTOAATA				8649
TTTGAAGATT TAAATCTGA CTCTAGGACG GGCACGCTGG CTCACGACTA TAATCCCAAC				8709
ACTTTGGGAG GCTGAGGCGG GCGGTACAAA GTTCAGGAAT TCAAAGACCAO CCTGACCAAT				8769
ATGGTGAAC CCCATCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGCAGGTGCC				8829
TOTAAGTCCC AGCTAGCTGT TGAGGTGAGG ATTGCATTGA GCCAAGATC				8878

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Arg	Met	Val	Ser	Trp	Ser	Phe	His	Lys	Leu	Lys	Thr	Met	Lys	
1				5					10					15		
His	Leu	Leu	Leu	Leu	Leu	Leu	Cys	Val	Phe	Leu	Val	Lys	Ser	Glu	Gly	
			20					25					30			
Val	Asn	Asp	Asn	Glu	Glu	Gly	Phe	Phe	Ser	Ala	Arg	Gly	His	Arg	Pro	
		35					40					45				
Leu	Asp	Lys	Lys	Arg	Glu	Glu	Ala	Pro	Ser	Leu	Arg	Pro	Ala	Pro	Pro	
	50				55						60					
Pro	Ile	Ser	Gly	Gly	Gly	Tyr	Arg	Ala	Arg	Pro	Ala	Lys	Ala	Ala	Ala	
	65			70				75						80		
Thr	Glu	Lys	Lys	Val	Glu	Arg	Lys	Ala	Pro	Asp	Ala	Gly	Gly	Cys	Leu	
			85					90						95		
His	Ala	Asp	Pro	Asp	Leu	Gly	Val	Leu	Cys	Pro	Thr	Gly	Cys	Glu	Leu	
		100					105						110			
Glu	Glu	Ala	Leu	Leu	Glu	Glu	Glu	Arg	Pro	Ile	Arg	Asn	Ser	Val	Asp	
		115				120						125				
Glu	Leu	Asn	Asn	Asn	Val	Glu	Ala	Val	Ser	Glu	Thr	Ser	Ser	Ser	Ser	
	130				135						140					
Phe	Glu	Tyr	Met	Tyr	Leu	Leu	Lys	Asp	Leu	Trp	Glu	Lys	Arg	Glu	Lys	
	145			150				155						160		
Glu	Val	Lys	Asp	Asn	Glu	Asn	Val	Val	Asn	Glu	Tyr	Ser	Ser	Glu	Leu	
			165					170						175		

605410: 834250

[illegible]

(2) INFORMATION FOR SEQ ID NO-5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(v i i) IMMEDIATE SOURCE:

- (B) CLONE: human fibrinogen protein chain

(i x) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
.. 2603, 4211..4341, 4643..4778, 5758..5942, 7426
.. 7703, 9342..9571)

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(X1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AAAAAGTTAG	CAAGATGTAA	TTATCAGTGT	ACTATGTAAA	TCTTTGTGAA	TGATCAATAA	120
TTACATATTT	TCATTATATA	TATTTTAGTA	GATAATATTT	ATATACATTG	AACATTCTAA	180
ATATAGAAAAG	TTTACAGAGA	AAAATAAAAG	CTTTTTTICC	AATCCTGTCC	TCCACCTCTG	240
CATCCCATTC	TTCTTCACAG	AGGCAACTGA	TTCAAGTCAT	TACATAAGTA	TTGAGTGTTA	300
ACTACAACATA	TGTTAAGTAC	AGCTATATAT	GTTAGATGCC	GTAAGCCACA	AAATCAATTT	360
ACAATCTAAT	GCAAGTGGATA	CAAGCATGAT	ACATATAATA	TAAAGTTGCT	ACAAATGCTA	420
TCTGAGGTAG	AGCTGTTTTG	AAAGAACTA	ATACTTAAAT	GTTTAATTCA	ACTGACTTGA	480
TTGACAACCTG	ATTAGCTGAG	TGGAAAAAGT	GGATGAGAAA	GATTGTGAGA	CTTAATTGOC	540
TGGTGGTATG	GTOATATGAT	TOACAATAAC	TGCTAAATCA	GAGAGGGATA	TATTAAGGAG	600
GAGAGAGAAA	GCAACAAATC	TGTTTTGAT	GTGTTCACTT	TGTTATAATT	ATGATTATT	660
TACTGAATAT	GAATATTTAT	CTTTGTTTTT	GAGTCAATAA	ATATACCTTT	GTAAAGACAG	720
AATTAAGATA	TTAGTATTTT	TTTCAAACTG	GAGGCATTTT	TCCCACTAAC	ATATTTTATC	780
AAAACCTATA	ATAAGCTTGG	TTCCAAGGGA	AGAAATGAGG	GATAACCAAA	AATAAGAGCA	840
TTAATAATAG	TGTAACGCCC	AGTGATAAAT	CTCAATAAGC	AGTGATGACA	GACATGTTTT	900
CCCAAAACACA	AGGATGCTGT	AAAGGCCAAA	CAAGAAATGAT	GGCCCCCTCC	CAAGACCTCA	960
TTTTGCCCTT	TCCTTCACT	ATGCTCTAC	TCTCCTTTAG	ATACAAAGGA	GGTGGATTTT	1020
TCTCTTCTCT	GAGATAAGCT	GATGGAACCA	CAAGAAACAA	GAAATGGGCT	CCTGGCTCTT	1080
TTCTCTGTGG	CAAGATGGGT	GCCATGCCCC	CCTTCAAGACA	AAAGGAAAGT	TGAAGCTCAA	1140
AGCTCCCTGA	GAAATGAGAG	CCTATGAACA	TGTTTGACAC	AGAGGGAGCA	GAATGTATTT	1200
CCAGGGTCAT	TCATTCCCTG	GAATAATGAA	CTGGGACATG	GGGGAAATCA	GTCTCCTCCT	1260
GCCACAAGCA	CAAGTTAAAA	ATAATAATGT	TAACTGATCC	CTAGGCTAAA	ATAATAATGT	1320
TAACTGATCC	CTAAGCTAAG	AAAGTTCTTT	TGTAATTCA	GGTGAATGGA	GCAAGACCCA	1380
TCTTAAGGAT	AGACTAAGTT	TGCTTAAGTT	GAGGTCATAT	CTGTTTGCTC	TCAAGCATGT	1440
ACTGGAAGAA	GTTGATCAC	ACAGCCTCCA	GGACTGCCCT	CCTCCTCACA	GCAATGGATA	1500
ATGCTTCACT	AGCCTTTGCA	GATAATTTTG	GATCAGAGAA	AAAACCTTGA	GCTGGGGCAA	1560
AAAGGAGGAG	CTTCAACCTG	TGTGCAAAAT	CTGGGAACCT	GACAGTATAG	GTTGGGGGGC	1620
AGGATGAGGA	AAAAAGAACG	GGAAAAACCT	GGCCACCCCT	CTGGTAAGGA	GGCCCCGTGA	1680
TCAAGTCCAG	CCATTTGCA	TGCTGGCTAT	CCCAAGAGCT	TACATAAAGG	GACAATTGGA	1740
GCCTGAGAGG	TGACAGTGT	GACACTACAA	GGCTCGAGGC	TCCGGGCACT	CAAGACATC	1798
ATG AGT TGG TCC TTG CAC CCC CGG AAT TTA ATT CTC TAC TTC TAT GCT	1846					
Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala						
1 5 10 15						
CTT TTA TTT CTC TCT TCA ACA TOT GTA GCA GTAAATGTGC TCTTCACAAA	1896					
Leu Leu Phe Leu Ser Ser Thr Cys Val Ala						
20 25						
ACGTTGTTTA AAATGGAAG CTGAAAAATA AAACAGATAA TAAACTAGTG AAATTTTCGT	1956					
ATTTTTTCTC TTTTAA TAT GTT GCT ACC AGA GAC AAC TGC TGC ATC TTA	2005					
Tyr Val Ala Thr Arg Asp Asn Cys Cys Ile Leu						
30 35						
GAT GAA AGA TTC GTAAATAGTT TTTATGTTTC TCCCTTTGTG TGTGAACCTG	2057					
Asp Glu Arg Phe						

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40

AGAGGGGCGCA	AGGAATAGAA	ATAATTCCCT	CATAAATATC	ATCTGCGACT	TGTAACATTTT	2117
TAAAAACATA	GTCTAGGTTT	TACCTATTTT	TCTTAATAOA	TTTTAAGAGT	AGCATCTGTC	2177
TACATTTTTA	ATCACTGTTA	TATTTTCAO	GGT AGT TAT	TGT CCA ACT ACC	TGT	2230
			Gly Ser Tyr	Cys Pro Thr Thr Cys		
				45		
GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT	2278					
Gly Ile Ala Asp Phe Leu Ser Thr Tyr Glu Thr Lys Val Asp Lys Asp						
50 55 60 65						
CTA CAG TCT TGG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA	2326					
Leu Glu Ser Leu Glu Asp Ile Leu His Glu Val Glu Asn Lys Thr Ser						
70 75 80						
GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT	2374					
Glu Val Lys Glu Leu Ile Lys Ala Ile Glu Leu Thr Tyr Asn Pro Asp						
85 90 95						
GAA TCA TCA AAA CCA A GTGAGAAAAT AAAGACTACT GACCAAAAAA	2420					
Glu Ser Ser Lys Pro						
100						
TAATAATAAT AATCTGTGAA GTTCTTTTGC TGTTTTTTTA GTTGTTCIAT TTGCTTAAGG	2480					
ATTTTTATGT CTCTGATCCT ATATTACAG AT ATG ATA GAC GCT GCT ACT TTG	2532					
	Asn Met Ile Asp Ala Ala Thr Leu					
	105 110					
AAG TCC AGG ATA ATG TTA GAA GAA ATT ATG AAA TAT GAA GCA TCG ATT	2580					
Lys Ser Arg Ile Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile						
115 120 125						
TTA ACA CAT GAC TCA AGT ATT CG GTAAAGGATTT TTGTTTTAAT TTGCTCTGCA	2633					
Leu Thr His Asp Ser Ser Ile Arg						
130						
AGACTGATTT AGTTTTTATT TAATATTCTA TACTTGAGTG AAAGTAATTT TTAATGTGTT	2693					
TTCCCCATTT ATAATATCCC AGTGACATTA TGCCGTGATTA TGTGAGGCAT AGTAGAGATA	2753					
GAAATTTTTA GTGCAATATA AATTATACTG GTTTATAAAT GCTTATTAAT AATCACATTO	2813					
AAAGAAAAGATG TTCTAGATGT CTTCAAAATGC TAOTTTGACC ATATTTATCA AAAATTTTTT	2873					
CCCCATCCCC CATTTATCTT ACAACATAAA ATCAATCTCA TAGGAATTTG GTGTGTTGAAA	2933					
ATAAAATCCT CTTTATAAAA ATGCTGACAA ATTGTTGTTT AAAAAAATTA GCAAGCAGAG	2993					
GCATAGTAAG GATTTTGCGT CCTAAAGTAA ATTATATTGA ATGTGGAOCA GGAAGAAACA	3053					
TGTCTTGAGA GACTAAAGTG GCGAAATATT GCAAAAGCTCA TATGATCAT TCGAAGATGA	3113					
ACCTGCATAG TCTCTTCCCT TCATTTGAAA GTGAATGTCT CTGTTAAAAG TTCTCAAGGA	3173					
CTCATAAACT TTCTGAACAT AAAGTCTCAO ATACAGTTTT AATATTTTTT CCCAATTTTT	3233					
TTTTCTGAAT TTTTCTCAAA GCAAGCTTGAO AAATTOAGAT AAATAATAOC TAGGGAAGAAO	3293					
TGCCCCAAGA AAGATTTCTC CTCTTTTTTC TATCAAGAGG CCCTTOTTAT TATTOTTATT	3353					
ATTATTACTT GCATTATTAT TGTCCATCAT TGAAGTTGAA GGAAGTTATT GTACAGAAAT	3413					
TGCTTAAGAC AAGGTAGAGG GAAAAAGTGG ACAAATAATT TGTCTACCCT TTTTACTTC	3473					
AAAGAAAAGAA CGTTTTATGC ATTGTAGACA GTTTTCTATC ATTTTTGAGT ATTTGCAAGC	3533					
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TGTAACCAAG AOCATTAAGG AAAGAAAAGGG AAGTATCTGT TTTTTTATT TACATACAA	3653					
ACOTTCCAAG ATCATGTCCC TGTGTAAATT ATATTTTGA TGAAGCTTA TATGTATAOC	3713					
CTCAOTAGAT CCACAAGTGA AAGGTATACT CCTTCAAGCAC ATGTGAATTA CTGAAGTGAO	3773					

[illegible]

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GGTTOCTATC	TOCTOTCCCT	TATOCATAAA	GTAAAAAGCA	AAATOTCAAT	OACATTTGCT	3893							
TATTOACAAG	GACTTTGTTA	TTTGTGTTGG	GAGTTOAGAC	AATATOCCTC	ATTCTAAOTA	3953							
AAAAAGATTCA	GGTCCACATT	GTATTCCTGT	TTTAATTGAT	TTTTTGATTT	GTTCCTTTCT	4013							
TTCAAAAAAGT	TTATAATTTT	AATTCATOTT	AATTTAGTAA	TATAATTTTA	CATTTTCCTC	4073							
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AAATATAAAA	TTACTCTTCT	GAAAGGAATA	CTTATTTTTG	TCTTCTTATT	TTTGTATCT	4193							
TATGTTTCTG	TTTGTAG A	TAT TTO	CAO GAA	ATA TAT	AAT TCA	AAT AAT CAA	4244						
		Tyr	Leu	Gla	Gla	Ile	Tyr	Asa	Ser	Asa	Asa	Gla	
		135					140					145	
AAG ATT GTT	AAC CTG	AAA GAG	AAG GTA	GCC CAG	CTT GAA	GCA CAG	TGC						4292
Lys Ile Val	Asa Leu	Lys Gla	Lys Val	Ala Gla	Leu Gla	Ala Gla	Cys						
	150			155			160						
CAG GAA CCT	TGC AAA	GAC ACO	GTG CAA	ATC CAT	GAT ATC	ACT GGG	AAA G						4341
Gla Gla Pro	Cys Lys	Asp Thr	Val Gla	Ile His	Asp Ile	Thr Gly	Lys						
	165			170			175						
GTAACTGATG	AAGGTTATAT	TOGGATTAGG	TTCATCAAAO	TAAOTAATOT	AAAAGGAGAAA	4401							
GTATOTACTG	GAAAOTATAG	GAATAOTTTA	GAAAOTGOGT	ACCCATTAAO	TCTAAGAAAT	4461							
TCAOTTTGTCT	AGACCTTTCT	TOAATAGCTA	AAAAAAACAO	TTTAAAAOGA	ATOGTGTOT	4521							
GAAAAOTAAO	AAAATTATTC	TTGGAAAAATG	AATAGTTTAC	TACATOTTAA	AAOCTATTTT	4581							
TCAAGOGCTOG	CACAGTCTTA	CCTOCATTTT	AAACCACAGT	AAAAOTCGAT	TCTCCTTCTC	4641							
TAG AT TOT	CAA GAC	ATT GCC	AAT AAG	GGA OCT	AAA CAG	AOC GGG	CTT					4688	
Asp Cys	Gla Asp	Ile Ala	Asa Lys	Gly Ala	Lys Gla	Ser Gly	Leu						
	180			185			190						
TAC TTT ATT	AAA CCT	CTG AAA	GCT AAC	CAG CAA	TTC TTA	GTG TAC	TOT					4736	
Tyr Phe	Ile Lys	Pro Leu	Lys Ala	Asa Gla	Gla Phe	Leu Val	Tyr Cys						
	195			200			205						
GAA ATC GAT	GGG TCT	GGA AAT	GGA TGG	ACT GTG	TTT CAG	AAO						4778	
Gla Ile Asp	Gly Ser	Gly Asa	Gly Trp	Thr Val	Phe Gla	Lys							
	210		215			220							
GTAAATTTTTT	CCCCACCATO	TGTATTTAAT	AAATTCCTAC	ATTGTTTCTG	CCATATGACA	4838							
GATACTTTTC	TAAOCACCTT	GTAAACCOTA	GCTCATTTAA	TCCTTTOCAAT	AGCCCTAAGG	4898							
GGAAAGTACT	TCTGTTACTC	CTATTTACAG	AAAAAGAAAC	TGAAGCACAC	AAAGTTAAAT	4958							
AACTTOCCCA	AGACCACATA	ACTAATAAGC	AACAGAGTCA	GCATTTGAAC	CTAAGCAOTA	5018							
TAGTTTCAOA	GTTTGTOACT	TOACTCTATA	TTOTACTGOC	ACTOACTTTG	TAGATTCTAO	5078							
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AGGTCAAAGAC	CTGAGGTTTC	CCATCACAAO	ATGAGGAAAG	CCAACACCAC	CCCCCACCAC	5198							
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GGAACTTGTG	TTGCATCTGC	CACCTGCTGA	TACCCACTAG	GAATCTTGGC	TCCTTTACTT	5318							
TCTGTTTACC	TCCCACCACCT	GTATTAAGTG	TTTCTACAGG	GGGCGCTCAG	AGGGAATGAA	5378							
TGGTGGAAAG	ATTAAGTTGCC	AGACACCOAT	TGAGCAATGG	GTTCATCAT	AAOTGTAAGG	5438							
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GATCCTTTOCA	GCAACCCTAA	GAAOTAACCA	TCATTTTTTC	TATTTGATAC	ATGAGGAAAC	5618							
TGAAGTACGT	TGCCCAAGAT	CACCTAAGTT	GGAGTTGATA	GAACCACTGC	TCTGTATTTT	5678							
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CTTGCAAATG TOTAATTAG AGA CTT GAT GGC AGT GTA GAT TTC AAG AAA AAC	5790
Arg Leu Asp Gly Ser Val Asp Phe Lys Lys Asa	
225 230	
TGG ATT CAA TAT AAA GAA GGA TTT GGA CAT CTG TCT CCT ACT GGC ACA	5838
Trp Ile Glu Tyr Lys Glu Gly Phe Gly His Leu Ser Pro Thr Gly Thr	
235 240 245	
ACA GAA TTT TGG CTG GGA AAT GAG AAG ATT CAT TTG ATA AGC ACA CAG	5886
Thr Glu Phe Trp Leu Gly Asa Glu Lys Ile His Leu Ile Ser Thr Glu	
250 255 260 265	
TCT GCC ATC CCA TAT GCA TTA AGA GTG GAA CTG GAA GAC TGG AAT GGC	5934
Ser Ala Ile Pro Tyr Ala Leu Arg Val Glu Leu Glu Asp Trp Asa Gly	
270 275 280	
AGA ACC AG GTACTGTTTT GAAATGACTT CCAACTTTTT ATTGTAAAGA	5982
Arg Thr Ser	
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GCAAACAGCA CATCCAQCCA CCATTTTCTC CAGGAGTCTG TTTGGTTCTT GGGCAATCCA	6102
AAAAAGGTAAA TTCTATTCAQ GATGAATCTA AGTGTATTGG TACAATCTAA TTACCCTGGA	6162
ACCATTTCAGA GTAATAQCTA ATTACTGAAC TTTTAATCAG TCCCAGGAAT TGAGCATAAA	6222
ATTATAATTT TATCTAGTCT AAATTACTAT TTCAAGAAAGC AAGTATTATT ATTAATCCCA	6282
TTTTATAQAT TAACTTGCTC AAAATCACAT TGCTGATAAG TGGTAGAGGT AGAATTCAQA	6342
CTCAAQTAQT TTAACTTTAA AGCCTGTCTT CTTAACAACCT ATCCTGGTTO AAAAGCAAAAT	6402
ACAQCCTCTT CAQACTTCTC AGTGCCITTA TGGCCATTTA TTCTGTCAAA TCATGAQCTA	6462
CCCTAAAAAT AAACCAQCTA GCTCTTTTGA TGATCTAGAG GCTTCTTTTT GCTTGAQATA	6522
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AAQAAAAATCC CTTTAGCACC TAACCCITTA GGTGCTATGA GTGQCTAATG GAACGTATACC	7002
TCCTTCAAQT TTTGTGCAAT AATTAAQGGT CACTCACTGT CAQATACTTT CTGTGATCTA	7062
TGATAATGTO TGTGCAACAC ATAACATTTT AATAAAAAQA GAAAAATATGA AATTAGAGTC	7122
ATCTACACAT CTGQATTTGA TCTTAGAAATG AAACAAQCAA AAAAGCATCC AAGTGAQTGC	7182
AATTATTAQT TTTCAQAGAT GCTTCAAAGG CTCTAGGCC CATCCCGGGA AGTGTTAATG	7242
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ATGAGCAAAAT TTCAQCCTTA AQAACAAAAQ TCAAAAAATTC CAAGQAAQCA TCCTACQAAA	7362
GAQGGAACTT CTGAGATCCC TGAGGAGGGT CAQCATGTGA TGGTTGTATT TCCTTCTTCT	7422
CAQ T ACT GCA GAC TAT GCC ATG TTC AAG GTG GGA CCT GAA GCT GAC	7468
Thr Ala Asp Tyr Ala Met Phe Lys Val Gly Pro Glu Ala Asp	
285 290 295	
AAG TAC CQC CTA ACA TAT OCC TAC TTC OCT GGT GGG GAT OCT GGA GAT	7516
Lys Tyr Arg Leu Thr Tyr Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp	
300 305 310	
OCC TTT GAT GGC TTT GAT TTT GGC GAT GAT CCT AQT GAC AAG TTT TTC	7564
Ala Phe Asp Gly Phe Asp Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe	
315 320 325 330	

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ACA	TCC	CAT	AAT	GGC	ATG	CAO	TTC	AOT	ACC	TGG	GAC	AAT	GAC	AAT	GAT	7612
Thr	Ser	His	Asn	Gly	Met	Gln	Phe	Ser	Thr	Trp	Asp	Asn	Asp	Asn	Asp	
				335					340					345		
AAO	TTT	GAA	GGC	AAC	TGT	GCT	GAA	CAO	GAT	GGA	TCT	GGT	TGG	TGG	ATG	7660
Lys	Phe	Gln	Gly	Asn	Cys	Ala	Gln	Gln	Asp	Gly	Ser	Gly	Trp	Trp	Met	
			350					355					360			
AAC	AAO	TGT	CAC	GCT	GGC	CAT	CTC	AAT	GGA	GTT	TAT	TAC	CAA	G		7703
Asn	Lys	Cys	His	Ala	Gly	His	Leu	Asn	Gly	Val	Tyr	Tyr	Gln			
		365					370					375				
GTATGTTTTT	CTTTCCTTAA	TTCCAAATTA	ATGTATAATG	TATACTATTT	TCATAAAAAA											7763
TAATAAATAG	ATATGAAAGAA	ATGAAAGAA	ATTTATAAAG	ATAATAAGGA	TTTTATCATG											7823
TTCTTTATTT	CAACTAAATT	CTTTGAAACT	GGAAATGGAT	AATACCAAGT	TCATGCCCTAA											7883
AATTAGCCCT	TCTAAAGAAA	TCCACCTGCT	GCAAAATATC	CAATAATTTG	GCATTATATG											7943
TGAAACTATC	ACCATCATAG	CTGGCACTGT	GGTTTGTGGG	ATCTCCTTTA	GACATACAAC											8003
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TTCCCATGAG	CTTTGTGTCA	GATACACGCA	GTGAAACAGT	GTTTGGAGGA	ACAGAAATAA											8123
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GAGGACAGTA	GACACTTATT	TTAGGATGGG	GGTTGGATGA	GGAGGCTATA	GTTCCTATA											8243
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GCCTTACCGA	TGCTAAAGGA	TCCATGTTAC	AATAATGGCA	TTATTTGGAA	ATCCCAATGG											8363
TATTCCATGA	ATAAAACCAC	TATGAAAGTA	ATCCCACTCA	ACAAGACTCT	COTTTGAGAA											8423
GGACAAGAAC	ACCACCTTGG	GAAAAGCCAA	CAATCAAGAC	AGACCTGTTT	AGCATCAATA											8483
GGACTTCCCT	ACCATATCTG	CTGGGTAGAT	GAATGAAACC	AGTGTTCCAA	ACCACCTCCG											8543
GCTTGTAGCA	AACCATAATC	TCTCATCTA	CCAAAGATGA	CAACCTTACC	TCCTGATGTC											8603
CTAGCCAATC	ACCAACTAAG	AAACTTTGCA	CAATTTATTT	AAAATTAACG	TTTGAATTTT											8663
ACAATATTTT	TAAATTTGAG	AAACATAACT	TATCTTTGCA	CTCACAAACC	ACATAATGAG											8723
AAGAAACTCT	AAGGAAAAAT	GCTTGTATCT	TGTGACCCCG	GGGCCCATGC	CAGAGCTGTA											8783
GTTCATGCCA	GTGTTGTGCT	CTGACAAAGC	TTTTACAGAA	TTACATGAG	TCTGCTTCCC											8843
TAGGACAAAG	AGAAAGCCAA	TCAACAGAGG	CTGCACTTTA	AAATGAGAGC	ATAAAATAAC											8903
ATGCCAGAAC	CATTTCCCTAA	AGCTCCTCAA	TCAACCAACA	AAATTTGTCT	TTCAAATAAC											8963
CTGAGTTGAC	CTCATCAAGG	ATTTTGTGGC	TCCTTCTCTT	CTAACCTGCC	TGAAAGAAAG											9023
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GGAGATATTT	TCAATTAAGC	GATAATACTA	TAAATTTTAT	GTAACTGGCA	ATGCACTTGG											9263
TAATAAGACG	CTCTTCATAG	ACTTGCAGAG	GTAAAAAGAT	TCCAGAAATA	TGATATGTAC											9323
ATCTACGACT	TGTTTTAG	GT GGC ACT	TAC TCA AAA	GCA TCT ACT	CCT AAT											9373
		Gly Gly Thr	Tyr Ser Lys	Ala Ser Thr	Pro Asn											
			380		385											
GGT TAT GAT AAT GGC ATT ATT TGG OCC ACT TGG AAA ACC CGG TGG TAT																9421
Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr Arg Trp Tyr																
	390						395				400					
TCC ATG AAG AAA ACC ACT ATG AAG ATA ATC CCA TTC AAC AGA CTC ACA																9469
Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn Arg Leu Thr																
	405					410					415					
ATT GGA GAA GGA CAG CAA CAC CAC CTG GGG GGA GCC AAA CAG GTC AGA																9517

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Ile Gly Glu Gly Glu Glu His His Leu Gly Gly Ala Lys Glu Val Arg
 420 425 430 435
 CCA GAG CAC CCT GCG GAA ACA GAA TAT GAC TCA CTT TAC CCT GAG GAT 9565
 Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr Pro Glu Asp
 440 445 450
 GAT TTO TAGAAAATTA ACTGCTAACT TCTATTOACC CACAAAATTCT 9621
 Asp Leu
 CTGAAAATTCT CTTCCTTTTT TCTCTTACTA TATTTATTGA TTTCAAGTCT TCTATTAAAG 9681
 ACATTTAGCC TTCAATGGAA ATTAAAACTC ATTTAAGGACT GTATTTCCAA ATTACTGATA 9741
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 AAAATACAGC AACCCAAACT GACAATACTC TATACAAGAA CATAATCACT AAGCAGGAGT 10521
 CACAOCACCA CAACCAAGAT GCATAGTATC CAAAGTGCAG CTG 10564

(2) INFORMATION FOR SEQ ID NO.:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.:

Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala
 1 5 10 15
 Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp
 20 25 30
 Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr
 35 40 45
 Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Glu Thr Lys Val Asp Lys
 50 55 60
 Asp Leu Glu Ser Leu Glu Asp Ile Leu His Glu Val Glu Asn Lys Thr
 65 70 75 80
 Ser Glu Val Lys Glu Leu Ile Lys Ala Ile Glu Leu Thr Tyr Asn Pro
 85 90 95
 Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser
 100 105 110
 Arg Ile Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr
 115 120 125
 His Asp Ser Ser Ile Arg Tyr Leu Glu Glu Ile Tyr Asn Ser Asn Asn
 130 135 140

GAT T T O " G A G G A G G

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Gln	Lys	Ile	Val	Asn	Leu	Lys	Gln	Lys	Val	Ala	Gln	Leu	Gln	Ala	Gln
145					150					155					160
Cys	Gln	Gln	Pro	Cys	Lys	Asp	Thr	Val	Gln	Ile	His	Asp	Ile	Thr	Gly
				165					170					175	
Lys	Asp	Cys	Gln	Asp	Ile	Ala	Asn	Lys	Gly	Ala	Lys	Gln	Ser	Gly	Leu
			180					185					190		
Tyr	Phe	Ile	Lys	Pro	Leu	Lys	Ala	Asn	Gln	Gln	Phe	Leu	Val	Tyr	Cys
	195						200					205			
Gln	Ile	Asp	Gly	Ser	Gly	Asn	Gly	Trp	Thr	Val	Phe	Gln	Lys	Arg	Leu
210					215						220				
Asp	Gly	Ser	Val	Asp	Phe	Lys	Lys	Asn	Trp	Ile	Gln	Tyr	Lys	Gln	Gly
225					230					235					240
Phe	Gly	His	Leu	Ser	Pro	Thr	Gly	Thr	Thr	Gln	Phe	Trp	Leu	Gly	Asn
			245						250					255	
Gln	Lys	Ile	His	Leu	Ile	Ser	Thr	Gln	Ser	Ala	Ile	Pro	Tyr	Ala	Leu
			260					265					270		
Arg	Val	Gln	Leu	Gln	Asp	Trp	Asn	Gly	Arg	Thr	Ser	Thr	Ala	Asp	Tyr
	275						280					285			
Ala	Met	Phe	Lys	Val	Gly	Pro	Gln	Ala	Asp	Lys	Tyr	Arg	Leu	Thr	Tyr
	290					295					300				
Ala	Tyr	Phe	Ala	Gly	Gly	Asp	Ala	Gly	Asp	Ala	Phe	Asp	Gly	Phe	Asp
305				310						315					320
Phe	Gly	Asp	Asp	Pro	Ser	Asp	Lys	Phe	Phe	Thr	Ser	His	Asn	Gly	Met
			325						330					335	
Gln	Phe	Ser	Thr	Trp	Asp	Asn	Asp	Asn	Asp	Lys	Phe	Gln	Gly	Asn	Cys
			340					345					350		
Ala	Gln	Gln	Asp	Gly	Ser	Gly	Trp	Trp	Met	Asn	Lys	Cys	His	Ala	Gly
		355					360					365			
His	Leu	Asn	Gly	Val	Tyr	Tyr	Gln	Gly	Gly	Thr	Tyr	Ser	Lys	Ala	Ser
	370					375					380				
Thr	Pro	Asn	Gly	Tyr	Asp	Asn	Gly	Ile	Ile	Trp	Ala	Thr	Trp	Lys	Thr
385				390						395					400
Arg	Trp	Tyr	Ser	Met	Lys	Lys	Thr	Thr	Met	Lys	Ile	Ile	Pro	Phe	Asn
			405						410					415	
Arg	Leu	Thr	Ile	Gly	Gln	Gly	Gln	Gln	His	His	Leu	Gly	Gly	Ala	Lys
			420					425					430		
Gln	Val	Arg	Pro	Gln	His	Pro	Ala	Gln	Thr	Gln	Tyr	Asp	Ser	Leu	Tyr
	435						440					445			
Pro	Gln	Asp	Asp	Leu											
	450														

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ovine beta-1-microglobulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCGTGTGCG	ACCTGCAAGT	CAACGGAATCT	CTGTGTCTGT	TTTCATGTTA	GTACCACACT	60
GTGTTGTTG	CTGTAGCTTT	CAGCTACAGT	CTGAAATCAT	AAAACCTGTT	ACCTCCAAGT	120
CTGTTCTCTC	TCAAGATTGT	GTCTCTCTGT	TTGGGTCTTT	AGTGTCTCCA	CACAATTTTT	180

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AGAAATGTTT	GTCTAGTTC	TGTAAAAAAT	GATGCTGTA	TTTTGATAAG	GATTGCATTO	240
AATCTGTAAA	GCTACAGATA	TAGTCATTGG	GAGTACAGT	CACTTTAACA	ATATTAACTC	300
TTACATCTG	TGAGCATGAT	ATATTTTCCC	CCTCTATATC	ATCTTCAATT	CCTCCTATCA	360
GTTCCTTTCA	TTGCAATTTT	CTGAGTACAG	GTCTTACACC	TCCTTGGTTA	GAGTCATTCC	420
TCAGTATTTT	ATTCCCTTGA	TACAATTGTG	AATGAGGTAA	TTTTCTTAAT	TTCTCTTTCT	480
GATAGCTCAT	TGTTAGTGTA	TATATAGAAA	AGCAACAAGT	TTCTATGTAT	TAATTTTGTA	540
TCCTGCAACA	GATTTCTATG	TATTAATTTT	GTATCCTGCT	ACTTTACGGA	ATTCATTAT	600
TAGCTTTTTG	GTGACATCTT	GAGGATTTTC	TGAAAGAAAAT	GGCATGGTAT	GGTAAGACAA	660
GGTGTGATGT	CATCTGCAAA	CAGTGGCAGT	TTTCCTTCTT	CCCTTCCAAC	CTGGATTTC	720
TTGATTTCTT	TCTGTCTGAG	TACGACTAGG	ATTCCCAATA	CTATACCGAA	TAAAAAGTGG	780
AAAGAGTGGC	ATCCTTGTCT	TATTTTTCTG	ACCTTAGAGG	AAATGCTTTC	AGTTTTTCAC	840
CATTAAATAT	AATGTTTACT	GTGGGCTTGT	CATATGTGGC	CTTCATTATA	TGGAGGTCTA	900
TTCCCTCTAT	ACCCACCTTG	TTGAGAGTTT	TTATCATAAA	AGTATGTTGA	ATTTGTGCAA	960
AAATTTTTTC	TGCATCTATT	GAGATGATTT	TTACTCTTCA	ATTCATTAAT	GATTTTTATT	1020
CTTCATTTTG	TAAATGATTT	CCATTCTTCA	ATTTGTTAAC	GTGGTATATC	ACATTGATTG	1080
ATTTGTGGAT	ACCTTTGTAT	CCCTGGGATA	AACCTCACTT	GATCATGAGC	TTTCAATGTA	1140
TTTTTGAAAT	CACTTTGCTA	ATATTCTGTT	GGGTATTTTT	GCATCTCTAT	TCATCAATGA	1200
TATTTGGCTA	AGAAAAGTTT	TGTCTGGTTT	TAGTATCAAG	GTGATGCTGG	CCTCATAGAG	1260
AGAGTTTAGA	AGCATTTTCT	CCTCTTTGAT	TTTTCGGAAT	AGTTTGAATA	GGATAAGTAT	1320
TAACTCTTCT	TAAATGTTTT	GGGGACTTCC	CTGGTGAAGC	GGTGGTTGAG	AATCCGCTTC	1380
AGGGATGTGG	GTTTGATCCC	TGGTCAAGGA	ACCATTAAATA	AGATCCACAA	TGCTGCAAGC	1440
AACAAAGCCC	CAAAGCTGCA	CCACTGAGCT	GCAACCGCTG	CAGTGGCCAC	AGGCCACGAC	1500
CAGAGAAAGC	CCACATACAG	CAAGGAAAGC	CCAACACAAC	CGGAAAAAGG	AGTTTGGTGG	1560
AATACAGCTG	TGAAAGCCGC	TGGTCCCTGA	CTCCTGCTTG	AGGGAATTTT	TAAAAAATTA	1620
TTGATTCAAT	TTCAATTAAG	GTAACTGGTC	TGTTCAATAT	TTCTATTTCT	TCCGGGTTCA	1680
GTCTTGGGAG	ATTGTACATG	CCTAGGAATG	TGTCCGTTTC	TTCTAAGTTG	TCCATTTTAT	1740
TGGACATGCA	TGGGAGCACA	CAGCACCAGC	CAGCGAGACT	CATGCTGGCT	TCCTGGGGCC	1800
AGGCTGGGGC	CCCAAGGAGC	ATGGCATCCT	AGAGTGTGTG	AAAGCCCACT	GACCTGGCCC	1860
AGCCCCACAA	TTTCATTCTG	AGAAATGATT	CCTTGGCTTCT	GCACTTACAG	GGCCAAGATC	1920
TGACCTGCTT	CTGAGGAGCA	GGGGTTTTTG	CAGGACGGGG	AGATGCTGAG	AGCCGACGGG	1980
GGTCCAGGTC	CCCTCCCAAG	CCCCCTGTGC	TGGGGCAGCC	CTTGGGAAAG	ATTGCCCCAG	2040
TCTCCCTCCT	ACAATGTTCA	GTCCCAAGCT	CCCCAGGCCA	GAGCTGCTTT	ATTTCCGTCT	2100
CTCTCTCTGG	ATGGTATTTCT	CTGGAAGCTG	AAAGTTTCTG	AAATTATGAA	TAGCTTTGCC	2160
CTGAAAGGCA	TGGTTTGTGG	TCACGGTTCA	CAGGAACCTG	GGAGACCCTG	CAGCTCAAGC	2220
GTCCCGAGAT	TGGTGGCACC	CAGATTTTCT	AAAGTCGCTG	GGGAAACAGG	CGCTTGTTTT	2280
TCCCTGGCTG	ACCTCCCTCC	TCCCTGCATC	ACCCAGTTCT	GAAAGCAGAG	CGGTGCTGGG	2340
GTACAGGCTT	CTGCACTCTA	ACGGCGGTGT	CCAAACCACC	CGTGGTGGTG	TTGGGGGGGC	2400
TACCTATGGG	GAAAGGCTTC	TCACTGCAAT	GGTGGCCCCC	GTCCCTCTG	AGATCAAGAG	2460
TCCCAATCCG	GACGTCAAAAC	AGGGCGAGCT	CCCTCCAGAG	GCTCCAGGGA	GGGATCCTTG	2520
CCCCCCCCCT	GCTGGCTCCA	GCTCCTGGTG	CGGACCCCTT	GAGCCTGATC	TTGTAGAGCC	2580

CTCA0TCTA0	TCTCT0CCTC	C0T0TTCACA	C0CCTTCTCC	CCAT0TCCCC	TCC0T0TCCC	2640
C0TTTTCTCT	CACAA00ACA	CC00ACATTA	GATTA0CCCC	T0TTC0A0CC	TCACCT0AAC	2700
A0CTCACATC	T0TAAAGACC	TA0ATTCCAA	ACAA0ATTCC	AACCT0AA0T	TCCC00T00A	2760
T0T0A0TTCT	0000C0ACAT	CCTTCAACCC	CATCACAOCT	T0CA0TTCAT	C0CAAAAACAT	2820
00AACCT000	0TTTATC0TA	AAACCCAO0T	TCTTCAT0AA	ACACT0A0CT	TC0A00CCT0	2880
TT0CA0A0AT	TAAAG0T0CT	AATACAGATC	A000CAAG0A	CT0AA0CT00	CTAA0CCTCC	2940
TCTTTCCATC	ACAG0AAA00	0000CCT000	00C00CT00A	00TCT0CTCC	C0T0A0T0A0	3000
CTCTTTCCCT0	CTACAOCTAC	CAACA0TCTC	TCT000AA00	AAACCA0A00	CCA0A0A0CA	3060
A0CC00A0CT	A0TTTA00A0	ACCCCT0AAC	CTCCACCCAA	0AT0CT0ACC	A0CCA0C000	3120
CCCCCT00AA	A0ACCCTACA	0TTCAG0000	0AA0A0000C	T0ACCC0CCA	00TCCCT0CT	3180
ATCA00A0AC	ATCCCC0CTA	TCA00A0ATT	CCCCCACCTT	0CTCCC0TTC	CCCTATCCCA	3240
ATAC0CCCA0	CCCACCCCT0	T0AT0A0CA0	TTTA0TCACT	TAGAA0T0CA	ACT0AA00CT	3300
TTT0CATCCC	CTTT0CCA0A	00CACA000C	ACCCACA0CC	T0CT000TAC	C0AC0CCCAT	3360
0T00ATTCA0	CCA00A00CC	T0TCCT0CAC	CCTCCCT0CT	C000CCCCCT	CT0T0CTCA0	3420
CAACACACCC	A0CACCAGCA	TTCCCC0CT0C	TCCT0A00TC	T0CA00CA0C	TC0CT0TA0C	3480
CT0A0C00T0	T00A000AA0	T0TCCT000A	0ATTTAA0AT	0T0A0A00C0	00A00T000A	3540
00TT000CCC	T0T000CCT0	CCCATCCCA0	0T0CCT0CAT	TA0CCCCA0T	0CT0CTCA0C	3600
C0T0CCCCC0	CC0CA0000T	CA00TCACTT	TCCC0TCCCT0	000TTATTAT	0ACTCTT0TC	3660
ATT0CCATT0	CCATTTTT0C	TACCCTA0ACT	000CA0CA00	T0CTT0CAGA	0CCCTC0ATA	3720
CC0ACCA00T	CCTCCCTC00	A0CTC0ACCT	0AACCCCAT0	TCACCCCT0C	CCCAGCCT0C	3780
A0A000T000	T0ACT0CA0A	0ATCCCTTCA	CCCA000CCA	C00TCACAT0	0TTT00A00A	3840
0CT00T0CCC	AA00CA0A00	CCACCCCTCA	00ACACACCT	0TCCCCA0T0	CT00CTCT0A	3900
CCT0TCCCT0	TCTAA0A00C	T0ACCC000A	A0T0TTCCT0	0CACT00CA0	CCA0CCT00A	3960
CCCA0A0TCC	A0ACACCCAC	CT0T0CCCCC	0CTTCT0000	TCTACCA00A	ACC0TCTA00	4020
CCCA0A0000	ACTTCCCT0CT	T00CCTT00A	T00AA0AA00	CCTCCTATT0	TCCTC0TAGA	4080
00AA0CCACC	CC0000CCT0	A00AT0A0CC	AA0T000ATT	CC000AACCC	C0T00CT000	4140
00CCCA0CCC	000CT00CT0	0CCT0CAT0C	CTCCT0TATA	A00CCCCAA0	CCT0CT0TCT	4200
CA0CCCTCCA	CTCCCT0CA0	A0CTCA0AA0	CAC0ACCCCA	000ATATCCC	T0CA0CCAT0	4260
AA0T0CCCTC	T0CTT0CCCT	000CCT00CC	CTC0CCT0T0	0C0TCCA00C	CATCATC0TC	4320
ACCCA0ACCA	T0AAA00CCT	00ACATCCA0	AA00TTC0A0	00TT00CC00	0T000T0A0T	4380
T0CA000C00	0CA0000A0C	T000CCTCA0	A0A0CCAA0A	0A00CT0T0A	C0TT000TTC	4440
CCATCA0TCA	0CTA000CCA	CCT0ACAAAT	CCCC0CT000	0CA0CTTCAA	CCA00C0TTC	4500
ACT0TCTT0C	ATTCT00A00	CT00AA0CCC	AA0ATCCA00	T0TT00CA00	0CT00CTTCT	4560
CCT0C00CC0	CTCTCT0000	A0CA0AC00C	C0TCTTCTCC	A0TCCCT0T0	0C0CCCT0AT	4620
TTCTCTTTC	T0T0A00CCA	CCA00CCT0C	T00AAACAC0	CCT0CCT0C0	CA0CTTCACA	4680
C0ACCTTT0T	CATCTCTTTA	AA00CCAT0T	CTCCA0A0TC	AT0T0TT0AA	0TCT000000	4740
TTA0T000AC	ACA0TTCAGC	CCCTAAAA0A	0TCTCTCT0C	CCCTCAAAAT	TTCCCCACCT	4800
CCA0CCAT0T	CTCCCCAA0A	TCCAAAT0TT	0CTACAT0T0	000000CTCA	TCT000TCCC	4860
TCTTT000TT	CA0T0T0A0T	CT0000A0A0	CATTCCCCA0	00T0CA0A0T	T000000A0T	4920
ATCTCA000C	T0CCCCA00CC	0000T000AC	A0A0A0CCCCA	CT0T0000CT	00000CCCCCT	4980

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TCCCACCCCC	AGAOTGCAAC	TCAAAGTCCC	TCTCCAAGTG	GCAGGAGACTT	GGCACTCCTT	5040
GGCTATGGCG	GCCAGCGACA	TCTCCCTGCT	GGATGCCCCA	AGTCCCCCCC	TGAGAGGTGTA	5100
CGTGAAGGAG	CTGAAAGCCCA	CCCCCGAAGG	CAACCTGGA	ATCCTGCTGC	AGAAATGGTG	5160
GGCGTCTCTC	CCCAACATGG	AACCCCCACT	CCCCAGGGCT	GTGACCCCCC	CGGGGGGGTG	5220
GGTGAAGGAG	GGACCAAGGG	CCCCAGGGCT	GGGAAAGAGG	CTCAGAGTTT	ACTGGTACCC	5280
GGCGCTCCAC	CCAAAGGCTG	CCACCCAAGG	CTTTTTTTTT	TTTTAAACTT	TTATTAATTT	5340
GATGCTTCA	AACATCATCA	AACAAATGAA	CATAAAACAT	TCATTTTTGT	TTACTTGGAA	5400
GGGGAAGATA	AATCCTCTGA	AGTGGAAATG	CATAGCAAA	ATACATACAA	TGAGGCAAGT	5460
ATTCTGAATT	CCCTGTTAAT	CTAGGATTA	CAAGGTATAT	TGAGCAACAG	AGAGACATTT	5520
TCATCATTTT	TAGTCTGAAC	ACCTCAGTAT	CTAAAAATGA	CAAGAAAGTCC	TGGAAACGAA	5580
GCAGTGTGGG	GATAAGCCCC	TGTGAAAGCT	GCTGGGAGGC	AGCAGACCTG	GGTCTTCCGG	5640
CTCAAGCAGT	TCCCCTACCC	AGCCCTGTCC	ACCTCAGAGC	GGGGTCAAGG	TGCAAGGAGG	5700
AGCTGGATGG	GTGTGGGGGG	AGAGATGGGG	ACCTGAACCC	CAGGGCTGCC	TTTTGGGGGT	5760
GCCTGTGGTC	AAAGCTCTCC	CTGACCTTTT	CTCTCTGGCT	TCATCTGACT	TCTCTGGGCC	5820
CATCCACCCG	GTCCCCCTGT	GCCTGAAGTG	ACAGTGAAGT	CGCCGAGGCT	AGTTGGCCAG	5880
CTGGCTCCTA	TGCCCCATGC	ACCCCCCTCC	AGCCCTCCTG	GGCCAGCTTC	TGCCCCCTGC	5940
CCTCAAGTTA	TCCTGATGAA	AATGGTCCAT	GCCAATGGCT	CAGAAAGCAG	CTGTCTTTCA	6000
GGGAGAACGG	CGAGTGTGCT	CAGAAAGAGG	TTATTGCAAG	AAAAACCAAG	ATCCCTGCGG	6060
TGTTCAAAGT	CGATGGTGAG	TCCGGGTCCC	TGGGGGACAC	CCACCACCCC	CGCCCCCGGG	6120
GACTGTGGAC	AGGTTCAAGG	GGCTGGCGTC	GGGCCCTGGG	ATGCTAAAGG	ACTGGTGGTG	6180
ATGAAAGACAC	TGCTTGAACA	CCTGCTTCAC	TTGCTTCCCC	TGCCACCTGC	CGGGGGCCTT	6240
GGGGCGGTGG	CCATGGGCA	GTCCCCGGCT	GCGGGCTAAC	CCACCAAGGT	GACACCCGAG	6300
CTCTCTTTGC	TGGGGGGCGG	GCCTGCTCT	GGGCCCTCAG	GCTGAGCTCA	GGAGGTACCT	6360
GTGCCCCCTC	AGGGGTAAAC	GAGAGGCCGT	GGCCACTCCA	GGGGCCCAAG	TGCCCCACGA	6420
CCCCAGCCCC	CTCCACAGCT	CCTTCATCTC	CTGAGAGCAA	ACTCTGTCCG	CCCTCGCTCA	6480
TTCACTTGTT	CGTCCTAAAT	CGAGATGAT	AAAAGCTTCA	GGGGGGGTTG	GGGTTCATC	6540
AGGGCTGCCC	TTCCGCGGGG	CAGCCTGGGC	CACATCTGCC	CTTGGCCCCC	TGAGGACTCA	6600
CTCTGACTGG	AGCCCCTGCA	CTGACTGAGC	CCAAGGTGCC	CAGCCCAAGG	TCTCTGGCGC	6660
CATCCAGCTG	CAGTGGGTTT	GGGTGCTGGT	CCTGCCCCCA	AGCTGCCCCG	ACACCACAGG	6720
CAGCCGCGGG	TGCCCCACTG	CCTCGGTCA	GGTGAAGCCC	AGCTGCCCCC	GCTCAGGGCT	6780
TGCCCCGACA	ATGACCCCAT	CCTCAGGAGC	CACCCCCCTT	CCCTTGGCTG	GCAGTGTCCA	6840
GGCCCCACCC	AGATCGGGGG	AAAGCCTATT	TCTTGAACA	TCCAATCCCT	GGGGGAGGGG	6900
GCCTCAGACT	GAGTGGTGAG	TGTTCCCAAG	TCCAAGAGGT	GGTGAAGGGT	CCTGGCGGAT	6960
CCAAGATTGA	CAGTGAAGGG	TTCTTGGGGC	CCATGCGCCT	GGCAGTGGCA	GCAAGGAGAG	7020
GGAAAGACCA	TTTCAAGGGT	GGGGGATGCC	AGAGGCGCTC	CCACCCCGGT	CTTCGCGGGG	7080
TGGTGAACCC	GGGGGAGCCC	CGCTGGTGGT	GGAGGGTGGT	GGGGGCTGAC	TAGCAACCCC	7140
TCCCCCCCCG	TTGAAACTCA	CTTTTCTCCC	GTCTTGAACG	CGTCCAAGCT	TGAATGAGAA	7200
CAAAATCCTT	GTGCTGAGCA	CGAGTACAA	AAAATACCTG	CTCTTCTGCA	TGAAAGACAG	7260
TGCTGAAGCC	GAGCAAAAGC	TGGCCTGCCA	GTGCTTGGGT	GGGTGCCAAC	CCTGGCTGCC	7320
CAGGGAGACC	AGCTGCGTGG	TCCTTGGCTG	AACAAGGGGGT	GGGGGGTGGG	AGCTTGAATCC	7380

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CCAAGAGAG	GAGGGGTGG	GGTCCCTGA	GTCCCGCCAG	GAGAGAGTGG	TCCATACCG	7440
GGAGCCAATC	TCTGTGGGC	CTGTGGGTGG	CTGGGGACGG	GGGCCAGACA	CACAGGCCGG	7500
GAGACGGGTG	GGCTGCAAAA	CTGTGACTGG	TGTGACCCTC	GCATGGGGGC	CGGTGGTCAC	7560
TGAATCTAAC	AGCCTTTGTT	ACCGGGGAGT	TTCAATTATT	TCCCAAAATA	AGAACTCAAG	7620
TACAAAAGCA	TCTTTCAACT	ATCACATCCT	GAAAAACAAAT	GGCAGGTGAC	ATTTTCTGTG	7680
CCGTAGCAGT	CCCAGTGGGC	ATTTTCAAGG	CCCCTGTGCC	AGGGGGGGCG	GGGCATCGGC	7740
GAGTGGAGGC	TCCTGGCTGT	GTCAAGCCGG	CCAAGGGGAG	GAAAGGAGCC	GGACAGCCAG	7800
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AGACCACCTT	GGGGAGCAAG	GACTGACCCC	CGTCCCTGCC	CCATAATCAAG	GACCCCGGAG	7980
GTGGACAACG	AGGCCCTGGA	GAAATTGAC	AAAAGCCCTCA	AGGCCCTGCC	CATGCACATC	8040
CGGCTTGCTT	TCAACCCGAC	CCAAGTGGAG	GGTGAAGCACC	CAGGGGGGGC	CCTTCCCCAG	8100
GGCAGGAGGC	ACCCGGGGGG	GGGAGGAGCT	CCTCCCATGG	TGACCCCGAG	CTCCCCAGGC	8160
CTCCCAAGAG	GAAAGGGGTGG	GGTGCAGCAC	CCCCTGGGGG	CCCCCTCCCC	ACCCCTGCC	8220
AGGCCTCTCT	TCCCGAGGTG	TCCAATCCCA	TCCTGACCCC	CCCATGACTC	TCCCTCCCCC	8280
ACAAGGCAAT	GCCACGTCTA	GGTGAAGCCC	TGCCGGTGGC	TCTGGGGTAA	GCTGCTGCC	8340
CTGCCCCAGG	TCCTGGGCAC	ACACATGGGG	TAGGGGGTCT	TGGTGGGGGC	TGGGACCCCA	8400
CATCAGGCC	TGGGGTCCCC	CCTGTGAGAA	TGGCTGGGAG	CTGGGGTCCC	TCCTGGCGAC	8460
TGCAGAGCTG	GCTGGGGCGG	TGCCACTCTT	GTGGGTGACC	TGTGTCTGG	CCTCACACAC	8520
TGACCTCCTC	CAGCTCCTTC	CAGCAGAGCT	AAAGCTAAGT	GAGCCAGAAAT	GGTACCTAAG	8580
GGGAGGCTAG	CGGTCTTTCT	CCCGAGGAGG	GGCTGTCTGT	GAAACCACCA	CCATGGAGAG	8640
GCTGGCAAGG	GTCTGGCAAG	TGCCCCAGGA	ATCACAAGGG	GGCCCCATGT	CCATTTCAGG	8700
GGCGGGAGGC	CTTGGACTCC	TCTGGGGACA	GACGAGCTCA	CCACCGGGGG	CCCCCATCA	8760
GGGGGACTAG	AAAGGAGCA	GACTGCAATC	ACCCTTCTGT	GGACCCAGGC	CCCTCCAGGC	8820
CCCTCCTGGG	GCTCCTGCTC	TGGGCAAGCT	CTCCTTCACC	AATAAAAGCA	TAAACCTGTG	8880
CTCTCCCTTC	TGAGTCTTTO	CTGGAGCAGG	GGCAGGGGGT	GGAGAGAGTGG	TGGGAGGAGG	8940
GTCTGGCTCA	GAGGATGACA	GGGGGGCTGG	GATCCAGGGC	GTCTGCATCA	CAGTCTTGTG	9000
ACAAGTGGGG	GGCCACACAC	ATCACTGGGG	CTCTTTGAAA	CTTTCAAGAA	CCAAGGAGGG	9060
ACTGGGAGGA	GACATCTGCC	AGTTCACTTG	GAGTGTTCAG	TCAACACCCA	AACTCGACAA	9120
AGGACAGAAA	GTGGAAAAAT	GCTGTCTCTT	AGTCTAATAA	ATATTGATAT	GAAACTCAAG	9180
TTGCTCATGG	ATCAATATGC	CTTTATGATC	CAGCCAGCCA	CTACTGTGGT	ATCAACTCAT	9240
GTACCCAAAC	GCACTGATCT	GTCTGGCTAA	TGATGAGAGG	TTCCCAAGTGG	AGAGCTGGCA	9300
AGAGGTGACA	GTGAGAACTG	TCTGCACACA	CAGCAGAGTC	CACCAATCAT	CCTAAGGAGG	9360
TCAATCCTGG	TGTTCAATGG	AGGAGTGGAT	TGAAAGCTGA	AACTCCAATG	CTTTGGCCAC	9420
CTGATGTGAA	GAGCTGACTC	ATTTGAAAAA	ACCCGTGATC	TGGGAAAAAT	TGAGGGCAGG	9480
AGGAGAAAGG	GACGACAGAG	GATGAGATGG	TTGGATGGCA	TCACCAACAC	AATGGACATG	9540
GGTTTGGGGT	GACTCCAAGG	GTGGGTGATG	GACAGGGAGG	CCTGGCGTGC	TACGGAGGCG	9600
GTTTATGGGG	TCACAAAAGC	TGAGTGGCTG	AACTGAGCTG	AACTGAAATG	AAATGAGGTA	9660
TACAGCAAAAG	TGGGGATTTT	TTAGATAATA	AGAAATATACA	CATAACATAG	TGTATACTCA	9720
TATTTTATAT	CATACCTGAA	TGCTCAATCA	CTCAATCTGA	TCTGACTCTG	TGACCTATGG	9780

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ACCCTAGCCT	TCCAAGTTTC	TTCTGTCCAC	AGAAATTCCTC	AAAGCAAGAA	TACTGGAATG	9840
GGTAGCCATT	TCCTCCTCCA	GGGGATCCTC	CCGACCCAGG	GATTGAACCG	GCATCTCCTG	9900
TATTGCAAG	TGGATTCTTT	ACCACTGTGC	CACCAAGGAA	GCCCCTGTTA	CTCTCTATGT	9960
CCCACCTAAT	TACCAAAAGCT	GCTCCAAAGAA	AAAAGCCCCTG	TCCCCTCTGA	GCTTCCCAGC	10020
CTGCAGAGGG	TGGTGGGGGT	AGACTGTGAC	CTGGGAACAC	CCTCCCCTTT	CAGGACTCCC	10080
GGGCCACGTG	ACCCACAGTC	CTGCAGACAG	CCGGGTAGCT	CTGCTCTTCA	AGGCTCATTG	10140
TCTTTAAAAA	AAACTGAGGT	CTATTTTGTG	ACTTCGCTGC	CGTAACTTCT	GAACATCCAAG	10200
TGCGATGGAC	AGGACCTCCT	CCCCAAGCCT	CAAGGGCTTC	AGGGAGCCAG	CCTTCACCTA	10260
TGAGTCACCA	GACACTCGGG	GGTGGCCCCG	CCTTCAGGCT	GCTCACAATC	TTCCCATCGT	10320
CCTGATCAAA	GAGCAAGACC	AATGACTTCT	TAAGAGCAAG	CAGACACCCA	CAGGACACTG	10380
AGGTTACCA	GAGCTGAGCT	GTCCITTTGA	ACCTAAAGAC	ACACAAGCTCT	CGAAGGTTTT	10440
CTCTTAATC	TGGATTTAAG	GCCTACTTGC	CCCTCAAGAG	GGAAAGACAGT	CCTGCATGTC	10500
CCCCAGACAG	CCACTCGGTC	GCATCCGAGG	CCACTTAGTA	TTATCTGACC	GCACCCCTGA	10560
ATTAATCGGT	CCAAACTGGA	CAAAAACCTT	GGTGGGAAAT	TTCATCCCAAG	AGGCCTCAAC	10620
CATCCTGCTT	TGACCACCCT	GCATCTTTTT	TTCTTTTATG	TGTATGCATG	TATATATATA	10680
TATATATTTT	TTTTTTTTTC	ATTTTTTGGC	TGTGCTGGCT	GTTCGTTGCA	GTTCGGTGGC	10740
CAGGCTTCTC	TCTAGTTTCT	CTCTAGTCTT	CTCTTATCAC	AGAAGCAATCT	CTAGACGATC	10800
GACGCGT						10860

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTCCGATC GACGCGTCTGA CGATATACTC TAGACGATCG ACOCGTA

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

- (B) CLONE: BLGAMP3

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGATCCCTT GCCCCTGCTT CTGG

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

- (B) CLONE: BLGAMP4

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACGCGTCAT CCTCTGTGAG CCAG

24

G65716-3343660

-continued

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6839

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTACCTAGT

10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6632

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGACGCGGAT CCTACGTACC TGCAGCCATG TTTTCCATGA GG

42

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6627

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGGCTTCGG CAAGCTTCAG G

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6521

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCAAAAGACT TACTTCCCTC TAGA

24

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6520

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCATGAACGT CCGTGGTGG TTGTGCTACC

30

G C C T T G G C A A G C T T C A G G

-continued

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6519

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCACGCGAC GTTCATGCTC TAAAAACCGT

30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6518

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGCGGGAT CCTACGTACT AGGGGGACAG GGAAAGG

36

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6629

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGACGCGAAT TCTACGTACC TGCAGCCATG AAAAGGATGG TTTCT

45

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6630

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGACGCGAAT TCTACGTACC TGCAGCCATG AAACATCTAT TATTO

45

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (v i i) IMMEDIATE SOURCE:
 (B) CLONE: ZC6625

- (x i) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTGAAGATTT CAGATCTTGT C

21

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

(B) CLONE: ZC6626

(x i) SEQUENCE DESCRIPTION: SBQ ID NO-21:

AAGAATTACT GTGGCCTACC A

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

(B) CLONE: ZO6624

(x i) SEQUENCE DESCRIPTION: SBQ ID NO:22:

GCTGCGGAAT TCTACGTACT ATTGCTGTGG GAA

33

(2) INFORMATION FOR SBQ ID NO-23:

(i) **SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

(B) CLONE: ZC6514

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:23:

COACOCOOAT CCTACOTACC TOCAOCCATO AOTTOOTCCT TOCAC

45

(2) INFORMATION FOR SEQ ID NO-24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

(B) CLONE: 206517

(i i) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCTCTGGTA GCAACATACT A

21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

(B) CLONE: no6516

(x i) SEQUENCE DESCRIPTION: SBQ ID NO-23:

000TTTCTAO CCCTACTAOT AO

22

E

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v i i) IMMEDIATE SOURCE:

- (B) CLONE: sc6515

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

000TTTCTAG CCCTACTAGT AG

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCTACGG TCOATCGTCT AGAGTATATC GTCGACGCGT COATCGG

47

GAGTATATC